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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN FETAL LIVER

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human Fetal liver is described. Also described are single exon nucleic acid probes expressed in the Fetal liver and their use in methods for detecting gene expression.

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN FETAL LIVER

CROSS REFERENCE TO RELATED APPLICATIONS

5 The present application is a continuation-in-part of U.S.
patent application serial nos. 09/632,366, filed August 3,
2000 and 09/608,408, filed June 30, 2000; claims the
benefit under 35 U.S.C. s 119(e) of U.S. provisional patent
10 application serial nos. 60/236,359, filed September 27,
2000, 60/234,687, filed September 21, 2000, 60/207,456,
filed May 26, 2000, and 60/180,312, filed February 4, 2000;
and further claims the benefit under 35 U.S.C. s 119(a) of
UK patent application no. 0024263.6, filed October 4, 2000,
15 the disclosures of which are incorporated herein by
reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
REFERENCE THEREOF

20 The present application includes a Sequence Listing in
electronic format, filed pursuant to PCT Administrative
Instructions 801 - 806 on a single CD-R disc, in
triplicate, containing a file named pto_FETAL_LIVER.txt,
25 created 24 January 2001, having 25,630,231 bytes. The
Sequence Listing contained in said file on said disc is
incorporated herein by reference in its entirety.

Field of the Invention

30 The present invention relates to genome-derived
single exon microarrays useful for verifying the expression
of regions of genomic DNA predicted to encode protein. In
particular, the present invention relates to unique genome-
35 derived single exon nucleic acid probes expressed in human

Fetal liver and single exon nucleic acid microarrays that include such probes.

Background of the Invention

5 For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to
10 further the understanding of proteins - known or suspected - about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent
15 biological understanding.

 For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

 More recently, however, the development of high
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein
30 product.

 One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences - that is, those accessible through isolation of mRNA - are of greatest initial interest. This "expressed
35 sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams *et al.*,
Science 252:1651 (1991); Williamson, *Drug Discov. Today*
4:115 (1999)). For nucleic acids sequenced by this
approach, often the only biological information that is
5 known *a priori* with any certainty is the likelihood of
biologic expression itself. By virtue of the species and
tissue from which the mRNA had originally been obtained,
most such sequences are also annotated with the identity of
the species and at least one tissue in which expression
10 appears likely.

More recently, the pace of genomic sequencing has
accelerated dramatically. When genomic DNA serves as the
initial substrate for sequencing efforts, expression cannot
be presumed; often the only *a priori* biological information
15 about the sequence includes the species and chromosome (and
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence
accumulation by directed, EST, and genomic sequencing
approaches - and in particular, with the accumulation of
20 sequence information from multiple genera, from multiple
species within genera, and from multiple individuals within
a species - there is an increasing need for methods that
rapidly and effectively permit the functions of nucleic
sequences to be elucidated. And as such functional
25 information accumulates, there is a further need for
methods of storing such functional information in
meaningful and useful relationship to the sequence itself;
that is, there is an increasing need for means and
apparatus for annotating raw sequence data with known or
30 predicted functional information.

Although the increase in the pace of genomic
sequencing is due in large part to technological changes in
sequencing strategies and instrumentation, Service, *Science*
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),
35 there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of
5 a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium,
10 *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the
15 greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many
20 genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that
25 function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting
30 coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et
35 al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

Ismb 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset et al.,
5 *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence.
Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic
10 data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature*
15 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the expression of regions predicted to encode protein - readily
20 to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach
25 (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

30 It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries
35 targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5 . The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Diseases of the liver are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these
20 diseases; although causative mutations in single genes have been identified for some, these disorders are believed for the most part to have polygenic etiologies. There is a need for methods and apparatus that permit prediction of
25 diseases of the liver, particularly those diseases with polygenic etiology, from diagnosis of fetal liver.

Summary of the Invention

30 The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present invention also provides apparatus for verifying the
35 expression of putative genes identified within genomic

sequence.

In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human Fetal liver, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 12,673 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid

probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 25,129 or a complimentary sequence, or a portion of such a sequence.

5 Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

10 In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said
15 single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

 In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most
20 suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

 Preferably, a spatially-addressable set of single
25 exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

 Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The
30 nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride,
35 polytetrafluoroethylene, polystyrene, polycarbonate,

polyacetal, polysulfone, celluloseacetate,
cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is
provided a microarray comprising a spatially addressable
5 set of single exon nucleic acid probes in accordance with
the first aspect of the invention.

In one embodiment, a genome-derived single-exon
microarray is packaged together with such an ordered set of
amplifiable probes corresponding to the probes, or one or
10 more subsets of probes, thereon. In alternative
embodiments, the ordered set of amplifiable probes is
packaged separately from the genome-derived single exon
microarray.

In another aspect, the invention provides genome-
15 derived single exon nucleic acid probes useful for gene
expression analysis, and particularly for gene expression
analysis by microarray. In particular embodiments of this
aspect, the present invention provides human single-exon
probes that include specifically-hybridizable fragments of
20 SEQ ID Nos. 12,674 - 25,129, wherein the fragment
hybridizes at high stringency to an expressed human gene.
In particular embodiments, the invention provides single
exon probes comprising SEQ ID Nos. 1 - 12,673.

Accordingly, in a third aspect of the invention,
25 there is provided a single exon nucleic acid probe for
measuring human gene expression in a sample derived from
human Fetal liver which is a nucleic acid molecule
comprising a nucleotide sequence as set out in any of SEQ
ID NOs.: 1 - 12,673 or a complementary sequence or a
30 fragment thereof wherein said probe hybridizes at high
stringency to a nucleic acid expressed in the human Fetal
liver.

In one embodiment, a single exon nucleic acid
probe in accordance with the third aspect comprises a
35 nucleotide sequence as set out in any of SEQ ID NOs.:

12,674 - 25,129 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring
5 human gene expression in a sample derived from human Fetal liver which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 25,130 - 37,156 or a complementary sequence or a fragment thereof wherein said probe
10 hybridizes at high stringency to a nucleic acid expressed in the human Fetal liver.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous
15 nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

20 In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb,
25 preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or
30 PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first
35 member of a specific binding pair. Suitable fluorescent

labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single
5 exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks
10 homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance
15 with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is
20 provided a method of measuring gene expression in a sample derived from human Fetal liver, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said
25 first collection of nucleic acids derived from mRNA of human Fetal liver; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is
30 provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably
35 labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are derived from mRNA from the Fetal liver of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene, comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOs: 1 - 25,129 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOs: 12,674 - 25,129, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be encoded by a sequence comprising a sequence set out in any of SEQ ID NOS.: 1 -12,673.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ

ID NOS.: 25,130 - 37,156.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOs: 25,130 - 37,156, or fragment
5 thereof.

In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display
10 can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated sequence.

15 Detailed Description of the Invention

Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound
20 collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase
25 "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and
30 Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably
35 disposed on a plurality of beads, rather than on a unitary

planar substrate, as is described, *inter alia*, in Brenner
et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000);
in such case, the term "microarray" and phrase "nucleic
acid microarray" refer to the plurality of beads in
5 aggregate.

As used herein with respect to a nucleic acid
microarray, the term "probe" refers to the nucleic acid
that is, or is intended to be, bound to the substrate; in
such context, the term "target" thus refers to nucleic acid
10 intended to be bound thereto by Watson-Crick
complementarity. As used herein with respect to solution
phase hybridization, the term "probe" refers to the nucleic
acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising
15 SEQ ID NO.", and variants thereof, intends a nucleic acid
probe, at least a portion of which probe has either (i) the
sequence directly as given in the referenced SEQ ID NO., or
(ii) a sequence complementary to the sequence as given in
the referenced SEQ ID NO., the choice as between sequence
20 directly as given and complement thereof dictated by the
requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and
the equivalent acronym "ORF" refer to that portion of an
exon that can be translated in its entirety into a sequence
25 of contiguous amino acids i.e. a nucleic acid sequence
that, in at least one reading frame, does not possess stop
codons; the term does not require that the ORF encode the
entirety of a natural protein.

As used herein, the term "amplicon" refers to a
30 PCR product amplified from human genomic DNA, containing
the predicted exon.

As used herein the term "exon" refers to the
consensus prediction of the various exon and gene
predicting algorithms i.e. a nucleic acid sequence
35 bioinformatically predicted to encode a portion of a

natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.:. The codons encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least 10^7 , preferably at least 10^8 , more preferably at least 10^9 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

As used herein with respect to the visual display of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual

object of the display.

As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional
5 information.

Brief Description of the Drawings

10 The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the
15 functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the
20 process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

25 FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution,
30 among exons predicted according to the methods described, of expression as measured using simultaneous two color hybridization to a genome-derived single exon microarray. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or
35 more but not all tested tissues ("1" - "9"), or expressed

in all tissues tested ("10");

FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than $1e-30$ (1×10^{-30}) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

Methods and Apparatus for Predicting, Confirming, Annotating, and Displaying Functional Regions From Genomic Sequence Data

FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained

in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100
5 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger
10 contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was
15 erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession,
20 species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will
25 be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

30 Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the
35 National Institutes of Health and is maintained by the

National Center for Biotechnology Information (NCBI).
Databases of genomic sequence from species other than
human, such as mouse, rat, Arabidopsis, *C. elegans*, *C.*
briggsii, *Drosophila*, zebra fish, and other higher
5 eukaryotic organisms will also prove useful as genomic
sequence database 100.

Genomic sequence obtained by query of genomic
sequence database 100 is then input into one or more
processes 200 for identification of regions therein that
10 are predicted to have a biological function as specified by
the user. Such functions include, but are not limited to,
encoding protein, regulating transcription, regulating
message transport after transcription into mRNA, regulating
message splicing after transcription into mRNA, of
15 regulating message degradation after transcription into
mRNA, and the like. Other functions include directing
somatic recombination events, contributing to chromosomal
stability or movement, contributing to allelic exclusion or
X chromosome inactivation, and the like.

20 The particular genomic sequence to be input into
process 200 will depend upon the function for which
relevant sequence is to be identified as well as upon the
approach chosen for such identification. Process step 200
can be iterated to identify different functions within a
25 given genomic region. In such case, the input often will
be different for the several iterations.

Sequences predicted to have the requisite
function by process 200 are then input into process 300,
where a subset of the input sequences suitable for
30 experimental confirmation is identified. Experimental
confirmation can involve physical and/or bioinformatic
assay. Where the subsequent experimental assay is
bioinformatic, rather than physical, there are fewer
constraints on the sequences that can be tested, and in
35 this latter case therefore process 300 can output the

entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magnetooptical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or

interim form prior to passage to the succeeding process. Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

5 FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

10 The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene
15 prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding
20 regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences
25 and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be
30 determined is protein coding regions in human genomic sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements
35 of the subsequent analytical method. Alternatively, or in

addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate
5 criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

10 Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any
15 given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

20 Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given
25 BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated
30 into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are
35 typically updated on a frequent, even hourly, basis. Thus,

as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods
5 and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the
10 presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for
15 sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery
20 can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query,
25 depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by
30 process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

35 When query 20 returns sequence meeting the query

criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

5 Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

 Preprocessing 24 suitable for most approaches and
10 methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like.
15 Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

 Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence,
20 vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

25 Alternatively, or in addition, undesirable, including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies
30 a significantly higher than average density of known restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

35 Once identified, undesired sequence can be

removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X".

- 5 Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of
10 highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can
15 also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25.
20 Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion
25 from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the
30 informational requirements of the methods for effecting such identification, is followed by sequence processing 25, where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include,
35 but are not limited to, encoding protein, regulating

transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic
5 recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for
10 identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the
15 novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative
20 coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more
25 software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

30 As further described in Example 1, below, gene finding software programs yield a range of results. For the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region,
35 2% of the data analyzed; GENEFINDER was second, calling 1%;

and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although
5 discussed herein particularly with respect to exon calling, consensus among methods will in general increase reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be
10 repeated with a different method, with consensus among such iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as
15 well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated
20 and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene
25 prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way,
30 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be
35 identified is coding of protein sequence, and a first used

approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative
5 sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

10 Although shown as an iterative process, the multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

 Predicted functional sequence, optionally representing a consensus among a plurality of methods and
15 approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

 In the preferred embodiment of the methods of the present invention, wherein the function sought to be
20 identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

 For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into
25 putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-
30 specific ORFs can be chosen for subsequent use in gene expression assay.

 Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative
35 exon length, sequence GC content, existence of possible

secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using
5 amplified product, further considerations involving hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance
10 of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested
15 experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for
20 experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred
25 embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention
30 provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of
35 nucleic acid microarray, the genome-derived single exon

nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by
5 process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture
10 the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying
15 length.

However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the
20 methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can
25 alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or
30 intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about
35 300,400 or 500 bp in length, can be amplified. However, it

has been discovered that the percentage success at amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for

amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see

above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include

5 polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can

10 also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as

15 described in WO 98/12559.

The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by

20 presumed noncovalent interactions, or some combination thereof.

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version

25 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using

30 ink jet technology.

As is well known in the art, microarrays typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of

35 the present invention, a plurality of *E. coli* genes can

readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified
5 product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as
10 complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

15 Although particularly described herein as using high density microarrays constructed on planar substrates, the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined,
20 including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon,
25 and positively-charged derivatized nylon membranes. Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner *et al.*, *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No.
30 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however,
35 provide certain useful advantages, including high

throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon *et al.*, or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas *et al.*, *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure

expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries – and thus microarrays based thereupon – are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined – subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention – that is, the one third of sequences that had previously been accessioned in EST or other expression databases – are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse

transcription and cloning of unknown message in EST approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector

sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence.

With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without

such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned
5 material as probes in EST microarrays is that such microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of
10 the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of
15 probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon
20 microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

25 Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for
30 the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of human chromosome 22, Dunham *et al.*, *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of
35 human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, 5 in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved 10 using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of 15 differential splicing to tissue-specific expression patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used 20 for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention 25 typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the 30 exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides 35 the additional opportunity to assay prespliced RNA, and

thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely
5 constrained by inadequacies in the photolithographic synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be
10 performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered
15 (i.e., mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the
20 genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the
25 microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed
30 on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the
35 melting temperature of probes hybridized to their

complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the
5 microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ*
10 synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

15 The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

20 Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez et al., *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome
25 has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

30 Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as
35 *Saccharomyces cerevisiae*, particularly in genomic sequence

drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of
5 novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is
10 performed.

In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the
15 putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed
20 for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, *Reviewed in* Schena et al., and as further described in Example 2, below. The mRNA source for the
25 reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

30 mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be
35 measured) is reverse transcribed in the presence of

nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically
5 fluorometrically-distinguishable from the first label. As further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets,
10 hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage,
15 to process 500, where the results for each probe are related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it
20 is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally
25 as a solitary solid-phase or solution-phase probe, for further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially
30 identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well
35 of a microtiter dish. Although a 96 well microtiter plate

can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions
5 (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of
10 individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific
5' primers used for genomic amplification can have a first
15 common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the
20 amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of
25 agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of
30 probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable
35 media that provide probe identification and addressing

information, and that can additionally contain annotation information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

5 If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not
10 required.

The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived
15 microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

20 Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be
25 identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases,
30 such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any
35 sequence query algorithm, such as BLAST ("basic local

alignment search tool"). The results of such query -
including information on identical sequences and
information on nonidentical sequences that have diffuse or
focal regions of sequence homology to the query sequence -
5 can then be passed directly to process 500, or used to
inform analyses subsequently undertaken in process 200,
process 300, or process 400.

Experimental data, whether obtained by physical
or bioinformatic assay in process 400, is passed to process
10 500 where it is usefully related to the sequence data
itself, a process colloquially termed "annotation". Such
annotation can be done using any technique that usefully
relates the functional information to the sequence, as, for
example, by incorporating the functional data into the
15 record itself, by linking records in a hierarchical or
relational database, by linking to external databases, or
by a combination thereof. Such database techniques are
well within the skill in the art.

The annotated sequence data can be stored
20 locally, uploaded to genomic sequence database 100, and/or
displayed 800.

The methods and apparatus of the present
invention rapidly produce functional information from
genomic sequence. Coupled with the escalating pace at
25 which sequence now accumulates, the rapid pace of sequence
annotation produces a need for methods of displaying the
information in meaningful ways.

FIG. 3 shows visual display 80 presenting a
single genomic sequence annotated according to the present
30 invention. Because of its nominal resemblance to artistic
works of Piet Mondrian, visual display 80 is alternatively
described herein as a "Mondrian".

Each of the visual elements of display 80 is
aligned with respect to the genomic sequence being
35 annotated (hereinafter, the "annotated sequence"). Given

the number of nucleotides typically represented in an annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence
5 is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the
10 sequence.

As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored
15 electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically – for example, by time-delayed appearance of
20 a small overlaid window upon movement of a cursor or other pointer over rectangle 89 – or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user
25 specification of the genomic sequence to be displayed. Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or
30 alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene
35 name, or even a sequence returned by query for similarity

or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein.

For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

5 Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

10 Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction.
15 Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be
20 made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among
25 methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of
30 horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

35 Furthermore, field 81 can be used to show

predictions of a plurality of different functions.

However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as
5 a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including
10 interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right
15 borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of
20 annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing
25 an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using
30 genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe immobilized on the support surface of the microarray. As noted *supra*, such probe will often include a small amount of additional, synthetic, material incorporated during
35 amplification and designed to permit reamplification of the

probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity

has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to

indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

5 Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized
10 mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*.
15 BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by
20 DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates
25 unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of
30 such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present
35 invention rapidly produce functional information from

genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode
5 protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in
10 one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

15 Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray
20 hybridization analysis, the expression of 12,673 of these ORFs in Fetal liver.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in Fetal liver is currently
25 available for use in measuring the level of its ORF's expression in Fetal liver.

Diseases of the liver are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition,
30 onset, and/or aggressiveness of most, if not all, of these diseases; although causative mutations in single genes have been identified for some, these disorders are believed for the most part to have polygenic etiologies.

For example, cirrhosis is a major public health
35 problem. In the industrialized world, it is among the top

ten causes of death; among patients aged 45 to 65, it is the third leading cause of death. The high prevalence is largely the result of alcohol abuse, but other major contributors include chronic hepatitis, biliary disease and iron overload. Approximately 10-15% are cryptogenic.

Cirrhosis is a broad description encompassing the common end stage of many forms of liver injury. Many patients with cirrhosis will remain asymptomatic for years, while others show generalized weakness, anorexia, malaise, and weight loss or, occasionally, more severe symptoms.

The progression from fibrosis, an early consequence of liver disease, to cirrhosis, and the specific histologic morphology that characterizes cirrhosis depend on the extent of injury, the presence of continuing damage, and the response of the liver to damage. The liver may be injured acutely and severely (e.g. necrosis with hepatitis), moderately over months or years (e.g. biliary tract obstruction and chronic active hepatitis), or modestly but continuously (e.g. alcohol abuse).

During the repair process, new vessels connecting the hepatic artery and portal vein to the hepatic venules form within the fibrous sheath that surrounds the surviving nodules of liver cells. These vessels restore the intrahepatic circulatory pathway, but provide relatively low-volume, high-pressure drainage that is less efficient than normal and results in increased portal vein pressure (portal hypertension). Thus, cirrhosis is not static and its features depend on the disease activity and stage.

As cirrhosis is the end stage of many forms of liver disease, many genes have been identified that can contribute to the development of cirrhosis. These include, e.g., the genes responsible for Wilson disease (Online Mendelian Inheritance of Man ("OMIM") 277900), type IV glycogen storage disease (OMIM 232500), galactosemia (OMIM

230400), and a deficiency of alpha-1-antitrypsin (OMIM 107400). There is substantial evidence, however, for as yet uncharacterized loci which cause cirrhosis.

For example, Iber and Maddrey, *Prog. Liver Dis.* 2: 290-302 (1965), reviewed 13 previously reported families and 8 new to this study, each with 2 or more affected members. They pointed out that, with a single exception, the multiple cases were in the same generation. Within a given family, the age of onset, clinical course, and biopsy findings were very similar, but there were wide differences between families.

Kalra et al., *Hum. Hered.* 32:170-175 (1982) studied the families of 220 cases of Indian childhood cirrhosis and 70 families of age-matched controls. The hypotheses of autosomal recessive, partial sex-linkage, and doubly recessive inheritance were found untenable and the authors concluded that multifactorial inheritance was most plausible. Lefkowitz et al., *New Eng. J. Med.* 307:271-277 (1982) described 4 white American sibs who died between ages 4.5 and 6 years of cirrhosis that closely resembled that of the childhood cirrhosis of Asiatic Indians.

Another example of uncharacterized loci which cause cirrhosis are those related to the risk of alcoholism.

Cloninger, *Science* 236:410-416 (1987), defined two separate types of alcoholism. According to these definitions, type 1 alcohol abuse has its usual onset after the age of 25 years and is characterized by severe psychological dependence and guilt. Type 1 occurs in both men and women and requires both genetic and environmental factors to become manifest. By contrast, type 2 alcohol abuse has its onset before the age of 25; persons with this type of alcoholism are characterized by their inability to abstain from alcohol and by frequent aggressive and antisocial behavior. Type 2 alcoholism is rarely found in

women and is much more heritable.

Despite considerable effort to identify genes related to the risk of alcoholism, relatively few genes have been identified. Some of this work has suggested a
5 relationship between the metabolism of dopamine and alcoholism. Blum et al., J.A.M.A. 263:2055-2060 (1990) and Bolos et al., J.A.M.A. 264:3156-3160 (1990) investigated the relationship of the dopamine D2 receptor (DRD2; OMIM 126450) to alcoholism, but the sample size was small and
10 their results were inconclusive. However, Tiitonen et al., Molec. Psychiat. 4, 286-289 (1999), found a markedly higher frequency in a population of type 1 alcoholics of the low activity allele of the enzyme catechol-O-methyltransferase (COMT, OMIM 116790), which has a crucial role in the
15 metabolism of dopamine, suggesting a role for dopamine metabolism in increased risk of alcoholism. For a brief review of recent progress toward the identification of genes related to risk for alcoholism see Buck, Genome 9:927-928 (1998).

20 As another example, multiple genes have been shown to predispose to hyperlipoproteinemia or hyperlipidemia. Much attention has been focused on these disorders because there is a strong association of hyperlipidemia, especially hypercholesterolemia, with
25 development of coronary artery disease. Coronary artery disease accounts for at least 25% of all deaths in the United States. Coronary artery disease results when the arteries supplying the heart muscle become occluded by plaques composed of lipids like cholesterol, blood clotting
30 components and blood cells.

The major plasma lipids circulate bound to proteins as macromolecular complexes called lipoproteins. Although closely interrelated, the major lipoprotein classes - chylomicron, very-low-density lipoprotein (VLDL),
35 low-density lipoprotein (LDL), and high-density lipoprotein

(HDL) - are usually classified in terms of physicochemical properties (e.g., density after centrifugation). Chylomicrons, the largest lipoproteins, carry exogenous triglyceride from the intestine via the thoracic duct to the venous system and into peripheral sites. VLDL carries endogenous triglyceride primarily from the liver to the same peripheral sites for storage or use. Lipases quickly degrade the triglyceride in VLDL to produce intermediate density lipoproteins (IDL) and within 2 to 6 h, IDL is degraded further to generate LDL, which has a plasma half-life of 2 to 3 days. While the overall fate of LDL is unclear, the liver is responsible for removing approximately 70% and active receptor sites have been found on the surfaces of hepatocytes.

Several monogenic conditions that lead to elevated levels of one or more serum lipoproteins have been defined and the responsible gene identified, including, e.g., hyperlipoproteinemia type I (OMIM 238600), familial hypercholesterolemia (OMIM 143890), and familial defective apolipoprotein B (OMIM 107730). However, in many cases the etiology is unknown and there is strong evidence for additional uncharacterized loci.

For example, Zuliani et al., *Arterioscler. Thromb. Vasc. Biol.* 19:802-809 (1999) identified a Sardinian family with a recessive form of hypercholesterolemia with the clinical features of familial hypercholesterolemia (OMIM 603813), and found that previously identified genes were not responsible for this disorder. They proposed that in this new lipid disorder, a recessive defect causes a selective impairment of the LDL receptor function in the liver. Ciccarese et al., *Am. J. Hum. Genet.* 66:453-460 (2000) recently mapped this novel disease locus.

Another example is designated familial combined hyperlipidemia (OMIM 144250) which affects approximately 1-

2% of the population in the Western world. This disorder can have its basis in mutation in several novel genes, two of which have been mapped to chromosome 1 (Pajukanta et al., Nature Genet. 18:369-373 (1998)) and chromosome 11
5 (Aouizerat et al., Am. J. Hum. Genet. 65, 397-412 (1999)). The high frequency of this disorder suggests that most, if not all, hyperlipidemias are of multifactorial genetic etiology.

As yet a further example, primary schlerosing
10 cholangitis (PSC) is a disorder characterized by a patchy obliterative inflammatory fibrosis of the large bile ducts. Chronic inflammation leads to extensive bile duct strictures, cholestasis, and gradual progression to biliary cirrhosis. PSC occurs most often in young men and is
15 commonly associated with inflammatory bowel disease, especially ulcerative colitis. The onset is usually insidious, with gradual, progressive fatigue, pruritus, and jaundice. There is no specific therapy for sclerosing cholangitis, and liver transplantation is the only apparent
20 cure.

The etiology of PSC is not known, but both genetic and immunologic abnormalities have been implicated. However, the frequency of HLA-B8 and HLA-DT2, which are associated with a number of autoimmune diseases, is higher
25 in PSC than normal individuals. Prochazka et al., New Eng. J. Med. 322:1842-1844 (1990) found that 100% of 29 patients with primary sclerosing cholangitis carried the HLA-DRw52a antigen, which is normally present in 35% of the population.

30 As a still further example, sarcoidosis is a disease of unknown cause characterized by non-caseating granulomas in one or more organ systems. These granulomas may resolve completely or proceed to fibrosis. The disorder is systemic, but the liver is affected in approximately 75%
35 of cases. Sarcoidosis occurs mainly in persons aged 20 to

40 yr and is most common in Northern Europeans and American blacks. The lifetime risk of developing sarcoidosis is particularly high among Swedish men (1.15%), Swedish women (1.6%), and African Americans (2.4%).

5 The much greater frequency in African Americans relative to the United States population overall suggests a genetic contribution to etiology. Early research studying familial aggregation indicated that the disease may have a nongenetic basis because the family pattern did not conform
10 to a simple Mendelian mode of inheritance (Allison, Sth. Med. J. 57: 27-32 (1964)). However, Headings et al., Ann. N.Y. Acad. Sci. 278:377-385 (1976) favored multifactorial genetic inheritance of susceptibility. Nowack et al., Arch. Intern. Med. 147:481-483 (1987), found an unusually
15 high frequency of HLA-DR5 in a study of 440 patients with sarcoidosis in Marburg, Germany. They also concluded that the role of an environmental or infectious agent triggering sarcoidosis cannot be envisaged without considering genetically linked cofactors.

20 Other significant diseases of liver are also believed to have a genetic, typically polygenic, etiologic component. These diseases include, e.g., primary biliary cirrhosis, Zellweger syndrome, cholestasis-lymphedema syndrome, Alstrom syndrome, primary pulmonary
25 hypertension, Berardinelli-Seip congenital lipodystrophy, iron overload in Africa, neonatal cholestatic hepatitis, autosomal recessive KID syndrome, familial hypotransferrinemia, type I congenital dyserythropoietic anemia, porphyria variegata, Finnish lactic acidosis with
30 hepatic hemosiderosis, Rotor syndrome, essential hypertension, ARC syndrome, type II conjugated hyperbilirubinemia, Lambert syndrome, ichthyosis congenita with biliary atresia, Kabuki make-up syndrome, Meckel syndrome, cerebral aneurysm-cirrhosis syndrome, glycogen
35 storage diseases, polycystic kidney and hepatic disease,

isolated Caroli disease, trisomy 18-like syndrome, Osler-Rendu-Weber syndrome 3, fatal intrahepatic cholestasis, Coach syndrome, type C Niemann-Pick disease, hereditary persistence of fetal hemoglobin and hepatocellular cancer.

5 Altered responses to a variety of infectious agents that target the liver, especially acute viral hepatitis, have also been shown or are suspected to have genetic bases or contributions. In addition to differential susceptibility to primary infectious agents,
10 these altered responses include predisposition to complicating conditions following contact with particular infectious agents. These include, e.g., development of hepatocellular carcinoma 2 correlated with Hepatitis B infection, and severe hepatic fibrosis following
15 *Schistosoma mansoni* infection.

 The central role of the liver in drug metabolism results in exposure of this organ to a large variety of potentially toxic chemical agents and metabolites. These include naturally occurring plant alkaloids and mycotoxins,
20 industrial chemicals, and, additionally, pharmacologic agents used in treating disease. The range of manifestations of toxin- and drug-induced liver disease are virtually as broad as the range of acute and chronic disorders and have also been shown or suspected to have
25 genetic bases or contributions.

 Such interactions between drugs and genotype have been shown in the response, e.g., to the anticonvulsant phenytoin, which can cause severe hepatitis-like disease in individuals who are impaired in the ability to detoxify a
30 metabolite of phenytoin in the liver, and in the response to the drug sodium valproate, which can produce severe hepatotoxicity in certain individuals. The abnormal responses to both of these drugs are believed to be influenced by underlying genetic factors.

35 The human genome-derived single exon nucleic acid

probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human liver, particularly those diseases with polygenic etiology. With each of the single
5 exon probes described herein shown to be expressed at detectable levels in human liver, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

10 For example, diagnosis (including differential diagnosis among clinically indistinguishable disorders, such as cirrhosis), staging, and/or grading of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression
15 profiles known to be characteristic of a given liver disease, or to specific grades or stages thereof.

In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the
20 patient's liver to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly, using nucleic acids obtained directly or indirectly from transcripts expressed by liver of individuals with known liver disease. Methods for
25 quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single
30 exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of liver disease to be assessed through the massively parallel determination of
35 altered copy number, deletion, or mutation in the patient's

genome of exons known to be expressed in human liver. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

5 The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art – see Ausubel et al. and Maniatis et al. – each probe reports the level of expression of message specifically containing that ORF.

10 It should be appreciated, however, that the probes of the present invention, for which expression in the Fetal liver has been demonstrated are useful for both measurement in the Fetal liver and for survey of expression in other tissues.

15 Significant among such advantages is the presence of probes for novel genes.

 As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be
20 identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were
25 represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence
30 databases.

 Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes
35 that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and
5 for surveying gene expression in the human.

Gene expression analysis using microarrays -- conventionally using microarrays having probes derived from expressed message -- is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405,
10 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct
15 Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for
20 example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of
25 Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

30 Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al.,
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"Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers, *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell Carcinoma Using Combination of cDNA Subtraction and Microarray Analysis," *Oncogene* 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change, serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway of which the gene's expressed protein is a part. Analogously, where gene expression analysis is used to assess side effects of pharmacological agents - whether in lead compound discovery or in subsequent screening of lead compound derivatives - the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile

and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

The invention particularly provides genome-derived single-exon probes known to be expressed in Fetal liver. The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known amplification technique. One such technique additional to

PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and WO 00/15779. As is well understood, where the probes are
5 to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form
10 suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

Each discrete amplifiable probe can also be
15 packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific
20 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3'
25 primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present
30 invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived
35 single exon microarray of the present invention, the

genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however – that is, for use in a hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) – length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message – a subset of target sequence that is much reduced in complexity as compared to genomic sequence – even fewer nucleotides are required for specificity.

Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 12,674 – 25,129, respectively, for probe SEQ ID NOS. 1 – 12,673. The minimum amount of ORF required to be included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 12,674 – 25,129 individually by routine experimentation using standard high stringency conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human cot1 DNA, and 0.5 % SDS, in a

humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in

both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have
5 sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or
10 both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution
15 hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR[®]

20 Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or
25 enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for
30 hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

35 When provided as a collection of plural

individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is
5 obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second,
10 different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen
15 for the common attribute of expression in the human Fetal liver.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell
20 type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF
25 by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to
30 provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-
35 derived single-exon nucleic acid microarrays comprising a

plurality of probes known to be expressed in human Fetal liver. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group
5 consisting of SEQ ID NOS.: 1 - 12,673.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of
10 probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the
15 same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with
20 a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to
25 their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 12,673 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 12,674 - 25,129, that encodes
30 a protein domain. Thus, each of SEQ ID NOS. 1 - 12,673 can be used, or that portion thereof in SEQ ID NOS. 12,674 - 25,129 used, to express a protein domain by standard *in vitro* recombinant techniques. See Ausubel et al. and Maniatis et al.

35 Additionally, kits are available commercially

that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT™ Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X™ Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL™) System, New England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 12,674 - 25,129. Such amino acid sequences are set out in SEQ ID NOS: 25,130 - 37,156. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

30

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

35 Preparation of Single Exon Microarrays from ORFs Predicted

in Human Genomic Sequence

Bioinformatics Results

5 All human BAC sequences in fewer than 10 pieces
that had been accessioned in a five month period
immediately preceding this study were downloaded from
GenBank. This corresponds to ~2200 clones, totaling ~350
MB of sequence, or approximately 10% of the human genome.

10 After masking repetitive elements using the
program CROSS_MATCH, the sequence was analyzed for open
reading frames using three separate gene finding programs.
The three programs predict genes using independent
algorithmic methods developed on independent training sets:
GRAIL uses a neural network, GENEFINDER uses a hidden
15 Markoff model, and DICTION, a program proprietary to
Genetics Institute, operates according to a different
heuristic. The results of all three programs were used to
create a prediction matrix across the segment of genomic
DNA.

20 The three gene finding programs yielded a range
of results. GRAIL identified the greatest percentage of
genomic sequence as putative coding region, 2% of the data
analyzed. GENEFINDER was second, calling 1%, and DICTION
yielded the least putative coding region, with 0.8% of
25 genomic sequence called as coding region.

The consensus data were as follows. GRAIL and
GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and
DICTION agreed on 0.5% of genomic sequence, and the three
programs together agreed on 0.25% of the data analyzed.
30 That is, 0.25% of the genomic sequence was identified by
all three of the programs as containing putative coding
region.

ORFs predicted by any two of the three programs
("consensus ORFs") were assorted into "gene bins" using two
35 criteria: (1) any 7 consecutive exons within a 25 kb window

were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon

to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR[®] green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular

Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than 1×10^{-100}) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from 1×10^{-5} to 1×10^{-99}). The remaining 45% of

the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., *Nature Genet.* 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

10

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single

5 Exon Microarrays

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II enzyme. The reaction was incubated for 2 hours at 42°C. After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup column, increasing the number of ethanol washes to 5. Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30 μ l hybridization solution
5 containing 50% formamide, 5X SSC, 0.2 μ g/ μ l poly(dA), 0.2 μ g/ μ l human c_ot1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC,
10 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics
15 Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

Although the use of pooled cDNA as a reference
20 permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact,
25 both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when
30 signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is
35 presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data - that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-

05 to $1e-99$; black: E values $> 1e-05$).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective
5 tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

10 It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested
15 tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence
20 databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

25 Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The
30 data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (designated "unknown") upon query of existing EST, NR and SwissProt databases, and
35 shows in blue the normalized Cy3 signal intensity for all

sequence-verified products with a BLAST Expect value of less than $1e-30$ ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

5 As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

10 However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes
15 will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and
20 further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach
25 described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis
30 of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene
35 expression panel 24 human cDNAs) (OriGene Technologies,

Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology – which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays – to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain				
Microarray Sequence Name	Normal ized Signal	Expressi on Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca ²⁺ binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin

AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be
5 important in the central nervous system or brain. The exon

giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097
5 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3
10 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed
15 down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless
20 of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to
25 tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often
30 used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et
35 al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result

duplicated with the array. Other highly expressed chip
 sequences included a translation elongation factor 1 α
 (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-
 chromosome RNA-binding motif (Chai et al., *Genomics*
 5 49(2):283-89 (1998)) (AC007320-3). A low homology analog
 (AP00123-1/2) to a gene, DSCR1, thought to be involved in
 trisomy 21 (Down's syndrome), showed high expression in
 both brain and heart, in agreement with the literature
 (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

10 As a further validation of the approach, we
 selected the BAC AC006064 to be included on the array.
 This BAC was known to contain the GAPDH gene, and thus
 could be used as a control for the ORF selection process.
 The gene finding and exon selection algorithms resulted in
 15 choosing 25 exons from BAC AC006064 for spotting onto the
 array, of which four were drawn from the GAPDH gene. Table
 3 shows the comparison of the average expression ratio for
 the 4 exons from BAC006064 compared with the average
 expression ratio for 5 different dilutions of a
 20 commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 \pm 0.11	-1.85 \pm 0.08
Brain	-1.41 \pm 0.11	-1.17 \pm 0.05
BT474	1.85 \pm 0.09	1.66 \pm 0.12
Fetal Liver	-1.62 \pm 0.07	-1.41 \pm 0.05
HBL100	1.32 \pm 0.05	2.64 \pm 0.12
Heart	1.16 \pm 0.09	1.56 \pm 0.10
HeLa	1.11 \pm 0.06	1.30 \pm 0.15
Liver	-1.62 \pm 0.22	-2.07 \pm

Lung	-4.95 ± 0.93	-3.75 ± 0.21
Placenta	-3.56 ± 0.25	-3.52 ± 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known

exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION
5 identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene
10 (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the
15 reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease
20 inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb,
25 upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):
30 red = kallistatin protease inhibitor (P29622);
purple = plasma serine protease inhibitor (P05154);
turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

EXAMPLE 4Genome-Derived Single Exon Probes Useful For Measuring
Human Gene Expression

5

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be
10 expressed at significant levels in Fetal liver tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical
15 structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification
20 from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 12,673 single exon probes, each fragment corresponding to an extension product from one of the two amplification primers.)

25 The structures of the 12,673 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 12,673. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the
30 exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 12,674 - 25,129, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

35 As detailed in Example 2, expression was

demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the
5 signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

10 For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

15 Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations
20 are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered
25 to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean + (3*SD)) is used as the signal threshold qualifier for that
30 particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

35 The probes and their expression data are

presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human Fetal liver and thus presents the subset of probes that was recognized to be
5 useful for measuring expression of their cognate genes in human Fetal liver tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 12,674 to 25,129 was individually used as a BLAST (or, for SWISSPROT, BLASTX)
10 query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenic hits from NR were scored.

15 The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as
20 "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the
25 SEQ ID NO.: of the exon contained within the probe:"EXON SEQ ID NO.:" from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of
30 the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is
35 found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS.

corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS.:. The
5 peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each
10 prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs
15 in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for
20 each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as
25 provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about $1e-05$ and $1e-100$), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

30 Using BLAST E value cutoffs of $1e-05$ (i.e., 1×10^{-5}) and $1e-100$ (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of $1e-30$ was used as the boundary when only two classes were to be defined for
35 analysis (unknown, $>1e-30$; known $<1e-30$) (see also FIG. 8).

Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about $1e-100$ – which is probative evidence that the query sequence has previously been shown to be expressed – the top hit is highly unlikely
5 exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present
10 identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached
15 sequence listing. For each amplicon probe (SEQ ID NOs.: 1 – 12,673) and probe exon (SEQ ID NOs.: 12,674 – 25,129, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

(a) the accession number of the BAC from which
20 the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST
25 E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

(d) the most similar sequence provided by BLASTX
30 query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

EXAMPLE 5

35 Genome-Derived Single Exon Probes Useful For Measuring

Expression of Genes in Human Fetal liver

Table 4 (526 pages) presents expression, homology, and functional information for the genome-derived single exon
5 probes that are expressed significantly in human Fetal liver.

CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived
5 from human Fetal liver comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 12,673 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
3. A spatially-addressable set of single exon nucleic acid
15 probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
4. A spatially-addressable set of single exon nucleic acid
20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 12,674 - 25,129.
5. A spatially-addressable set of single exon nucleic acid
25 probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
6. A spatially-addressable set of single exon nucleic acid
30 probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
7. A spatially-addressable set of single exon nucleic acid
35 probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single-exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.

12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human Fetal liver comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 12,673 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human Fetal liver.

35

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 12,674 - 25,129 or a complementary sequence or a fragment thereof.
- 5
15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human Fetal liver which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any
- 10 of SEQ ID NOs.: 25,130 - 37,156, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human Fetal liver.
- 15 16. A single exon nucleic acid probe as claimed in any one of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.
- 20 17. A single exon nucleic acid probe as claimed in any one of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.
18. A single exon nucleic acid probe as claimed in any one
- 25 of claims 13 - 17, wherein said probe is DNA, RNA or PNA.
19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.
- 30
20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.
- 35 21. A single exon nucleic acid probe as claimed in any one

of claims 13 - 20, wherein said probe lacks homopolymeric stretches of A or T.

22. A method of measuring gene expression in a sample
5 derived from human Fetal liver, comprising:
 contacting the microarray of claim 12, with a first
 collection of detectably labeled nucleic acids,
 said first collection of nucleic acids derived
 from mRNA of human Fetal liver; and then
10 measuring the label detectably bound to each probe of
 said microarray.

23. A method of identifying exons in a eukaryotic genome,
comprising:
15 algorithmically predicting at least one exon from
 genomic sequence of said eukaryote; and then
 detecting specific hybridization of detectably labeled
 nucleic acids to a single exon probe,
wherein said detectably labeled nucleic acids are derived
20 from mRNA from the Fetal liver of said eukaryote, said
probe is a single exon probe having a fragment identical in
sequence to, or complementary in sequence to, said
predicted exon, said probe is included within a microarray
according to claim 12, and said fragment is selectively
25 hybridizable at high stringency.

24. A method of assigning exons to a single gene,
comprising:
 identifying a plurality of exons from genomic
30 sequence according to the method of claim 23; and
 then
 measuring the expression of each of said exons in a
 plurality of tissues and/or cell types using
 hybridization to single exon microarrays having a
35 probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

5 25. A nucleic acid sequence as set out in any of SEQ ID Nos: 1 - 25,129 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of SEQ ID Nos: 1 - 25,129.

10

27. A peptide comprising a sequence as set out in any of SEQ ID Nos: 25,130 - 37,156.

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
475	13108	25800	4.41				
922	13535	26053	8.9				
1083	13688		2.9				
1345	13940	26462	10.32				
1656	14248	26782	2.59				
1678	14270	26803	5.03				
1763	14353	26898	1.73				
1785	14375	26919	0.99				
1792	14382	26927	9.24				
1935	14519	27075	1.21				
2021	14603	27168	3.24				
2210	14786	27360	4.38				
2318	14880	27465	2.04				
2607	15169	27735	0.89				
2607	15169	27738	0.89				
3220	15832	28311	1.65				
3496	16101	28576	1.22				
3566	16170	28652	10.28				
3617	16220		0.8				
3718	16319	28787	0.97				
4020	16618		0.94				
4275	16861	29310	1.53				
4348	16935	29376	8.4				
4368	16955	29396	0.74				
4368	16955	29397	0.74				
4430	17016		1.3				
4862	17537	29979	1.04				
5007	17580		0.59				
5054	17627	30071	0.61				
5197	17762	30187	5.95				
5212	17777	30198	1.32				
5482	18087	30415	2.1				
5482	18097	30416	2.1				
5615	18244		5.64				

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5783	18408		9.03				
5859	18244		4.85				
5910	18532	31257	0.84				
5915	18537	31282	3.16				
6173	24759	31552	1.41				
6200	18810	31579	1.65				
6548	19146		1.28				
6668	19284	32067	1				
6668	19284	32068	1				
7178	19711	32559	1.13				
7178	19711	32560	1.13				
7441	19865	32831	1.4				
7441	19865	32832	1.4				
8005	20547	33451	1.65				
8422	20962	33878	1.45				
8784	21333	34257	0.57				
8784	21333	34258	0.57				
9453	21879	34931	4.84				
9681	22180	35155	0.78				
9786	22294	35277	1.19				
9836	22431	35408	1.03				
10214	22709	35702	0.48				
10214	22709	35703	0.48				
10326	22820	35815	0.65				
10326	22820	35816	0.65				
10883	23099		3.06				
10725	24789	36268	2.46				
10906	23425		2.99				
11238	23769	36827	2.73				
11336	23034	36043	1.87				
11336	23034	36044	1.87				
11374	23826		2.59				
12117	24376		2.19				
12439	24576	30914	1.6				

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descripbr
6203	18813	31583	14.37	9.9E+00	AJ239028.1	NT	Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18
7948	20480	33400	1.65	9.8E+00	U32716.1	NT	Haemophilus influenzae Rd section 31 of 163 of the complete genome
9658	22157	35128	0.47	9.8E+00	Y18930.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
9658	22157	35129	0.47	9.8E+00	Y18930.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
7073	19845	32483	0.8	9.8E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
7073	19845	32484	0.8	9.8E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
10319	22813	35808	1.22	9.8E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor 1IH polypeptide 2 (Gtf2h2) genes, complete cds
10319	22813	35809	1.22	9.8E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor 1IH polypeptide 2 (Gtf2h2) genes, complete cds
2889	15247	27814	1.14	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2889	15247	27815	1.14	9.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2950	15566	28040	3.19	9.4E+00	AB043785.1	NT	Mus musculus A73 gene for antithrombin, complete cds
8042	20584	33491	0.99	9.3E+00	AF130980.1	NT	Homo sapiens ectodysplasin-A receptor protein (EDAR) gene, exons 2, 3, and 4
8933	21471	34390	3.48	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89)
5500	18134	30543	2.82	9.1E+00	AF095809.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5500	18134	30544	2.82	9.1E+00	AF095809.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
9351	21865		0.9	9.0E+00	P09241	SWISSPROT	RHODOPSIN
6196	18796	31584	5.12	8.9E+00	BE971806.1	EST_HUMAN	801651038R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934592 3'
6517	19117	31907	1.9	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster Cp Tbx3 premature mRNA, partial cds
6517	19117	31908	1.9	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster Cp Tbx3 premature mRNA, partial cds
465	13099	26590	1.68	8.4E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
9376	20315	33217	3.8	8.1E+00	AJ131718.1	NT	Zea mays mRNA for legumain-like protease (see 2a)
11048	23581		2.47	8.0E+00	P41920	SWISSPROT	BREFELDIN A RESISTANCE PROTEIN
8092	20633		0.76	7.6E+00	Z21489.1	NT	African swine fever virus NP1450L gene encoding RNA polymerase largest subunit
7364	19910		1.95	7.5E+00	AL445085.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
8302	20843	33784	1.54	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
8302	20843	33785	1.54	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5988	18589	31324	3.35	7.4E+00	BF700517.1	EST_HUMAN	802128878F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285508 5'
8688	21227	34147	2.63	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8688	21227	34148	2.63	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3006	15622	28098	3.19	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
3006	15622	28100	3.19	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
7097	19668	32507	0.7	7.2E+00	BE179060.1	EST_HUMAN	RCO-HT0613-200300-031-407 HT0613 Homo sapiens cDNA
7203	19734	32585	1.22	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7203	19734	32586	1.22	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
8516	22016		7.98	7.1E+00	AL181595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
11263	23781	35848	3.2	7.1E+00	P05850	SWISSPROT	HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION
9892	22389	33367	3.35	7.0E+00	P48610	SWISSPROT	ARGININE KINASE (AK)
11129	23637	35679	1.87	7.0E+00	O22469	SWISSPROT	WD-40 REPEAT PROTEIN MS13
8225	20766	33684	4.06	6.9E+00	P35679	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
10253	22748	35736	1.2	6.9E+00	P44834	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
7849	20391	33293	1.38	6.8E+00	W03412.1	EST_HUMAN	za07c11.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:291860 5'
7849	20391	33294	1.38	6.8E+00	W03412.1	EST_HUMAN	za07c11.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:291860 5'
9060	21597		1.13	6.8E+00	P36307	SWISSPROT	OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8]
10110	22605	35595	3.85	6.8E+00	Q03570	SWISSPROT	HYPOTHETICAL 157.0 KDA PROTEIN C38C10.5 IN CHROMOSOME III
5488	18122		0.69	6.8E+00	Q96028	SWISSPROT	CATECHOL-O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)
9886	22481	35465	1.89	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
9886	22481	35466	1.89	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
11008	23522		2.13	6.6E+00	Q10309	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE C8C3.05C
9108	21644	34584	7.21	6.5E+00	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
10206	22701	35695	0.49	6.5E+00	BE869001.1	EST_HUMAN	601878435F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3960989 5'
9657	22156	35127	1.11	6.2E+00	A Y010801.1	NT	Schizosaccharomyces commune unknown mRNA
10455	22949	35958	0.53	6.2E+00	6754621	NT	Mus musculus mannosidase 2, alpha B1 (Man2b1), mRNA
7102	19672	32511	1.34	6.0E+00	BE780163.1	EST_HUMAN	601468031F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3871303 5'
9730	22226	35205	0.48	6.0E+00	AF000008.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (817)
10407	22901	35896	0.6	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
10407	22901	35897	0.6	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
6643	19239	32042	6.67	5.9E+00	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk8) genes, complete cds
3576	16180		1.18	5.8E+00	7661557	NT	Homo sapiens DESCI1 protein (DESCI1), mRNA
7215	19746	32601	0.67	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
7215	19746	32602	0.67	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7570	20087		1.31	5.6E+00	P75080	SWISSPROT	DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLIII)
11349	23047	36059	2.86	5.6E+00	Q55276	SWISSPROT	LYOPENE BETA CYCLASE
6389	19002	31760	0.73	5.5E+00	P47447	SWISSPROT	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HIRCA
10658	23190		1.54	5.5E+00	AF175425.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 30, 31, and 32
11348	23046	36058	3.79	5.5E+00	P11690	SWISSPROT	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)
11578	24024		2.08	5.5E+00	AL161571.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 87
7008	19507	32326	1.2	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7009	19507	32327	1.2	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7369	19895		0.72	5.4E+00	Q96435	SWISSPROT	NEL PROTEIN PRECURSOR (NEL-RELATED PROTEIN 2)
7811	20354		1.58	5.4E+00	Q91062	SWISSPROT	VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1C; LIPOVITELLIN LV-2]
8734	21273	34193	0.78	5.4E+00	P40378	SWISSPROT	REP1 PROTEIN
8734	21273	34194	0.78	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
9849	22444	35423	1.33	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
9849	22444	35424	1.33	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
4899	17474	29830	1.52	5.3E+00	L43126.1	NT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
6614	19211		0.67	5.3E+00	P41779	SWISSPROT	HOMEOBOX PROTEIN CEH-20
8024	20566		3.71	5.3E+00	P54098	SWISSPROT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)
8914	21452		0.62	5.3E+00	AB034990.1	NT	Homo sapiens HERPUD1 gene for stress protein Herp, complete cds
5855	18282		1.04	5.2E+00	BE184840.1	EST_HUMAN	QV4-HT0891-270400-186-f09 HT0891 Homo sapiens cDNA
10274	22789		0.78	5.2E+00	AF248070.1	NT	Drosophila orientacea R1B retrotransposable element reverse transcriptase gene, partial cds
11074	23586		2.1	5.2E+00	Q10136	SWISSPROT	HYPOTHETICAL 61.1 KD PROTEIN C23E2.03C IN CHROMOSOME I
8892	21430	34354	0.88	5.1E+00	Q16005	SWISSPROT	RHODOPSIN
9739	22237	35217	0.97	5.1E+00	P08182	SWISSPROT	COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN)
9430	19033	31817	0.85	5.0E+00	BF510443.1	EST_HUMAN	601894910F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124114 5'
10096	22581		0.69	5.0E+00	BF308561.1	EST_HUMAN	601890420F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131509 5'
10327	22821	35817	3.37	5.0E+00	AF162445.2	NT	Canis familiaris skeletal muscle chloride channel ClC-1 (CLCN1) mRNA, complete cds
11170	23677	36723	13.54	5.0E+00	Z63860.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 103/162
10131	22626		0.71	4.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds
4135	16727		12.06	4.8E+00	AF185255.1	NT	Eunice australis histone H3 (H3) gene, partial cds
8095	20636	33547	0.65	4.8E+00	BF367909.1	EST_HUMAN	RC3-GN0042-100800-011-c10 GN0042 Homo sapiens cDNA
6478	21017		4.95	4.8E+00	AW750067.1	EST_HUMAN	PMO-BT0547-310100-002-b04 BT0547 Homo sapiens cDNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
311	12866	25454	1.88	4.7E+00	BF240592.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
312	12866	25454	1.68	4.7E+00	BF240592.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
3312	15923	28399	1.08	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
9124	21659	34601	1.09	4.6E+00	BE646437.1	EST_HUMAN	7e86g10.x1 NCL CGAP_CELL1 Homo sapiens cDNA clone IMAGE:3282098 3' similar to TR:O75140 O75140
9124	21659	34602	1.09	4.6E+00	BE646437.1	EST_HUMAN	KIAA0645 PROTEIN, contains element PTR5 repetitive element ; 7e86g10.x1 NCL CGAP_CELL1 Homo sapiens cDNA clone IMAGE:3282098 3' similar to TR:O75140 O75140
10280	22785		0.77	4.6E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
11474	23924	36894	1.99	4.5E+00	AE001044.1	NT	Archaeoglobus fulgidus section 63 of 172 of the complete genome
11596	24039	37108	1.67	4.5E+00	BF689841.1	EST_HUMAN	602123238F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280216 5'
3076	15691	28164	1.53	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284 5'
3076	15691	28165	1.53	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215284 5'
6349	18854		1.8	4.4E+00	X13414.1	NT	Murine I gene for MHC class II (la) associated invariant chain
6266	18874		0.82	4.3E+00	AF059679.1	NT	Homo sapiens neutrophil collagenase (CLGNA) gene, promoter region and 5'UTR
7464	19986	32851	2.36	4.3E+00	Y13402.1	NT	Plasmodium falciparum R28R+var1 gene, exon 1
7611	20124	33001	0.84	4.3E+00	AE001222.1	NT	Trapanema pallidum section 38 of 87 of the complete genome
10741	23266	36282	8.92	4.3E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
5708	18334		3.21	4.2E+00	P19444	SWISSPROT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-1) (RENAL DIPEPTIDASE) (RDP)
5780	18405	31121	1.46	4.2E+00	P51826	SWISSPROT	LAF-4 PROTEIN (LYMPHOID NUCLEAR PROTEIN)
6869	19603	32435	1.86	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
6869	19603	32436	1.86	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
8890	21428	34353	4.95	4.2E+00	A080913.1	EST_HUMAN	wf67g03.x1 Soares, NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2360692 3'
9832	22330	35312	2.07	4.2E+00	P31368	SWISSPROT	NUBIN PROTEIN (TWIN PROTEIN) (POU DOMAIN PROTEIN 1) (PDM-1) (DPOU-19) (DOCT1)
7166	19698	32545	0.81	4.1E+00	BE253688.1	EST_HUMAN	601107272F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351534 5'
7264	19792	32548	1.7	4.1E+00	BF247939.1	EST_HUMAN	601859030F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4069758 5'
7657	20169	33056	8.1	4.1E+00	O23810	SWISSPROT	YY1 PROTEIN PRECURSOR
7759	20267	33163	4.03	4.1E+00	P28964	SWISSPROT	GENE 88 PROTEIN
7759	20267	33164	4.03	4.1E+00	P28964	SWISSPROT	GENE 88 PROTEIN
7657	20399	33306	2.78	4.1E+00	U57503.1	NT	Pan troglodytes novel repetitive solo LTR element in the RNU2 locus
9459	21985	34939	0.63	4.1E+00	P11253	SWISSPROT	50S RIBOSOMAL PROTEIN L4
9590	22090	35054	2.26	4.1E+00	BF692425.1	EST_HUMAN	602247938F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333209 5'

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10208	22703		0.5	4.1E+00	P48414	SWISSPROT	CYCLIN-DEPENDENT KINASE INHIBITOR 1B (CYCLIN-DEPENDENT KINASE INHIBITOR P27) (P27KIP1)
10498	22883	36003	0.82	4.1E+00	O84242	SWISSPROT	3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE III (BETA-KETOACYL-ACP SYNTHASE III) (KAS III)
10765	23289		2.97	4.1E+00	P09716	SWISSPROT	HYPOTHETICAL PROTEIN HVLFI
10851	23372		13.84	4.1E+00	BE885880.1	EST_HUMAN	601607310F1 NIH_MGC_71 Homo sapiens cDNA IMAGE:3909051 5'
3599	16203		0.82	4.0E+00	P38229	SWISSPROT	GLC7-INTERACTING PROTEIN 1
5650	19515	32336	0.74	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
5650	19515	32337	0.74	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7017	19515	32336	0.95	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7017	19515	32337	0.95	4.0E+00	O62653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE; ISOMALTASE]
7240	19769	32625	1.34	4.0E+00	O33010	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
10070	22565	35560	0.6	4.0E+00	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
10156	22653	35647	0.49	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
10156	22653	35648	0.49	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
11423	23874	36837	3.99	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11423	23874	36938	3.99	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
3550	16154	28636	4.79	3.9E+00	X64518.1	NT	N. tabacum chitinase gene 50 for class I chitinase C
4413	16998		0.74	3.9E+00	AF055466.1	NT	Mus musculus seminal vesicle secretory protein 99 (MSVSP99) gene, promoter region
5839	19463	31186	3.08	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-H05 BN0070 Homo sapiens cDNA
5839	19463	31187	3.08	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-H05 BN0070 Homo sapiens cDNA
6748	19339	32145	0.71	3.9E+00	AF298209.1	NT	Dicotyledon discoidium non-LTR retrotransposon TRE5-B, polyprotein (gag) and group-specific antigen (pol) genes, complete cds
6792	19383	32198	0.72	3.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
6955	19532	32357	4.12	3.9E+00	P39299	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDB-RPSF INTERGENIC REGION
7398	19923	32787	6.09	3.9E+00	M23907.1	NT	Human MHC class II lymphocyte antigen (DPw4-beta-1) gene, exon 2

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8259	20800	33718	2.15	3.9E+00	X65865.1	NT	X.laavis mRNA for M4 muscarinic receptor
11269	23007	36014	3.27	3.9E+00	Y18000.1	NT	Homo sapiens NF2 gene
11291	23743	36800	1.62	3.9E+00	AA661489.1	EST_HUMAN	nt18a12.st NCI CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1168318 similar to gb:A10416
2658	15217		1.1	3.8E+00	AE001562.1	NT	METALLOPROTEINASE INHIBITOR 1 PRECURSOR (HUMAN);
6525	19125	31918	0.78	3.8E+00	Q57830	SWISSPROT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
8371	20911	33831	1.06	3.8E+00	D44725.1	EST_HUMAN	HYPOTHETICAL PROTEIN MJ0385
9710	22208		0.55	3.8E+00	AJ390861.1	NT	HUMSUPY135 Human brain cDNA Homo sapiens cDNA clone 148
4092	16687	28144	13.56	3.7E+00	AL161539.2	NT	Streptococcus oralis partial xpt gene for xanthine phosphoribosyltransferase, strain NGTC7984
7218	19749		0.79	3.7E+00	AL445065.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
							Thermoplasma acidophilum complete genome; segment 3/5
8642	21181		0.53	3.7E+00	4503950	NT	Homo sapiens glucokinase (hexokinase 4, maturity onset diabetes of the young 2) (GCK), nuclear gene encoding mitochondrial protein, mRNA
9105	21641	34581	0.88	3.7E+00	U43541.1	NT	Mus musculus leminin beta 2 gene, exons 17-33, and complete cds
11308	23801	36961	3.11	3.7E+00	BF68278.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
11308	23801	36862	3.11	3.7E+00	BF68278.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
11767	24158		1.28	3.7E+00	AB013746.3	NT	Gallus gallus mRNA for hypoxia-inducible factor-1 alpha, complete cds
619	13246	25719	2.6	3.6E+00	AV761055.1	EST_HUMAN	AV761055 MDS Homo sapiens cDNA clone MDSBUE10 5'
4917	17492		0.99	3.6E+00	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
8487	21026	33942	0.76	3.6E+00	D12367.1	EST_HUMAN	HUM0007B08 Liver HepG2 cell line. Homo sapiens cDNA clone tb08
8487	21026	33943	0.76	3.6E+00	D12367.1	EST_HUMAN	HUM0007B08 Liver HepG2 cell line. Homo sapiens cDNA clone tb08
8579	21118	34038	4.02	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
8579	21118	34039	4.02	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 8 of 529 of the complete genome
							Escherichia coli glycerophosphate dehydrogenase (glpD) gene, partial cds; and the translation start site has been verified (glpE), the translation start site has been verified (glpG), and repressor protein (glpR) genes, complete cds
10733	23259		4.32	3.6E+00	M98795.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
3284	15895	28373	1.08	3.5E+00	AF221538.1	NT	Borrelia burgdorferi (strain 25015) outer surface protein (ospC) gene, partial cds
6151	18764		1.06	3.5E+00	L42898.1	NT	Yg40c08.r1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:34940 5'
6360	18964	31742	0.92	3.5E+00	R19745.1	EST_HUMAN	THROMBOXANE-A SYNTHASE (TXA SYNTHASE) (TXS)
8421	20961		0.55	3.5E+00	P24557	SWISSPROT	
8962	21500	34421	0.88	3.5E+00	AA190998.1	EST_HUMAN	Zp86504.s1 Stralagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
8962	21500	34422	0.88	3.5E+00	AA190998.1	EST_HUMAN	Zp86504.s1 Stralagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
9414	21923	34872	1.12	3.5E+00	AL161553.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 53

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1558	14151	28683	4.49	3.4E+00	AF254577.1	NT	Brassica napus RP85d mRNA, complete cds
2612	15174	27742	1.02	3.4E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7397	19922	32786	2.85	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7690	20199	33086	0.86	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8611	21150		0.69	3.4E+00	U65406.1	NT	Human alternatively spliced potassium channels ROM-K1, ROM-K2, ROM-K3, ROM-K4, ROM-K5, and ROM-K6 (KCNJ1) gene, complete cds
8003	21540	34470	0.7	3.4E+00	AJ229042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
8040	21577	34506	0.5	3.4E+00	AJ250567.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 6
10165	22660	35655	3.61	3.4E+00	AF013197.1	NT	Saccharomyces cerevisiae MSS1 gene, complete cds
11408	23857	36922	1.98	3.4E+00	L7570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
6218	18828	31601	0.9	3.3E+00	Q08669	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
6218	18828	31602	0.9	3.3E+00	Q08669	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
7834	20376	33281	0.86	3.3E+00	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
10361	22855	35847	0.87	3.3E+00	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
10361	22855	35848	0.87	3.3E+00	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
526	13158	25640	1.72	3.2E+00	X86422.1	NT	D. rerio zp-50 POU gene
4088	13158	25640	0.7	3.2E+00	X86422.1	NT	D. rerio zp-50 POU gene
4835	17413	29866	1.24	3.2E+00		NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA
5757	18383	31095	1.34	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5757	18383	31096	1.34	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5787	18412	31128	2.45	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5787	18412	31129	2.45	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
6448	18049	31834	1.86	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
6448	18049	31835	1.86	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
7601	20114	32881	0.84	3.2E+00	P04275	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
7750	20258	33154	2.22	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
7750	20258	33155	2.22	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
8960	21498		4.84	3.2E+00	P13061	SWISSPROT	PERIPLASMIC [NIFE] HYDROGENASE SMALL SUBUNIT [NIFE HYDROGENLYASE SMALL CHAIN]
9448	21975	34927	1.52	3.2E+00	M36393.1	NT	S. cerevisiae threonine deaminase (LV1) gene, complete cds
10047	22542	35539	1.91	3.2E+00	AB016081.2	NT	Oryzias latipes OIGC6 gene for guanidyl cyclase C, complete cds
11727	24133		4.08	3.2E+00	L33838.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
8035	18654	31396	2.24	3.1E+00	Q10135	SWISSPROT	HYPOTHETICAL 142.6 KD PROTEIN C23E2.02 IN CHROMOSOME 1
7421	19945	32810	0.97	3.1E+00	P52178	SWISSPROT	TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID, PRECURSOR (CTPT)

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7711	20220		1.09	3.1E+00	AF303225.1	NT	Bacillus subtilis pectate lyase (pelE) gene, complete cds
8538	21077	33995	4.27	3.1E+00	P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE I 5DEIODINASE) (DIOI) (TYPE 1 DI) (SDI)
8538	21077	33996	4.27	3.1E+00	P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE I 5DEIODINASE) (DIOI) (TYPE 1 DI) (SDI)
9183	21760		3.77	3.1E+00	Q14957	SWISSPROT	GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9249	21775	34726	0.52	3.1E+00	Q01149	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9810	22308	35292	0.75	3.1E+00	7524759	NT	Chlorella vulgaris chloroplast, complete genome
9899	22396		0.56	3.1E+00	Q10125	SWISSPROT	HYPOETHICAL 56.3 KD PROTEIN F52C9.5 IN CHROMOSOME III
10239	22734	35726	4.7	3.1E+00	P49365	SWISSPROT	DEOXYHYPUSINE SYNTHASE (DHS)
11338	23036		2.91	3.1E+00	P33515	SWISSPROT	GENOME POLYPROTEIN[CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11355	23809		7.48	3.1E+00	S56680.1	NT	retinoid acid nuclear receptor isoform beta 2 [mice, embryonal carcinoma cell line, PC07-MZ1, mRNA, 2971 nt]
12490	24819		1.38	3.1E+00	U77666.1	NT	Brassica rapa pollen coat protein homodog (BAN103) gene, complete cds
5641	18173	30588	1.88	3.0E+00	X53096.1	NT	S. aureus gene encoding Sau961 DNA methyltransferase and Sau961 restriction endonuclease
6673	18269	32073	0.72	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
6673	18269	32074	0.72	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
7209	19740		10.44	3.0E+00	P18406	SWISSPROT	CYR61 PROTEIN PRECURSOR (3CH61)
7247	19776		0.77	3.0E+00	Q13201	SWISSPROT	ENDOTHELIAL CELL MULTIMERIN PRECURSOR
8838	21377		1.33	3.0E+00	X67838.1	NT	B. napus DNA for myosinase
10195	22860	35663	0.53	3.0E+00	Q58605	SWISSPROT	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)
10527	23064	36075	1.82	3.0E+00	Q16181	SWISSPROT	GDC10 PROTEIN HOMOLOG
10888	23409	36426	7.04	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
10888	23409	36427	7.04	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
2055	14636	27207	2.32	2.9E+00	AE002225.2	NT	Chlamydomonas reinhardtii AR39, section 53 of 94 of the complete genome
6224	18833		0.68	2.9E+00	AB026033.1	NT	Bonaparitia pedaliata mitochondrial DNA for 16S ribosomal RNA
6989	19487	32309	3.74	2.9E+00	Z36879.1	NT	F. pringlei gdcSpA gene for P-protein of the glycine cleavage system
7262	19790	32644	4.37	2.9E+00	Q14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR

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7282	19780	32845	4.37	2.9E+00	O1451.4	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7478	20001	32868	6.04	2.9E+00	P46589	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
7809	20352	33260	0.87	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPROTEIN [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
7809	20352	33260	0.87	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPROTEIN [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
8041	20583	33490	0.89	2.9E+00	BF344171.1	EST_HUMAN	802017413F1 NCL CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4153059 5'
1504	14086	26834	4.87	2.8E+00	AF186398.1	NT	Buxus harlandii maturase K (matK) gene, partial cds; chloroplast product
1675	14287		3.45	2.8E+00	AL161562.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
7348	19874	32740	4.88	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
9531	22031		0.57	2.8E+00	BE595182.1	EST_HUMAN	601342759F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3684807 5'
10568	19874	32740	1.68	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
251	12911	25394	9.31	2.7E+00	6878308	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
251	12911	25395	9.31	2.7E+00	6878308	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
5740	18368	31073	1.2	2.7E+00	L14005.1	NT	Homo sapiens apoA polymorphism K/ingle IV gene, exons 1 and 2
8088	20629		0.8	2.7E+00	U15947.1	NT	Ipomoea purpurea chalcone synthase (CHS) gene including complete 5'UTR and complete cds
8898	21438		1.68	2.7E+00	AL116459.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9353	20282	33191	0.83	2.7E+00	AW088191.1	EST_HUMAN	xc88e12.x1 NCL CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2591374 3' similar to gb:M17733
10394	22888		1.48	2.7E+00	BE063527.1	EST_HUMAN	THYMOSIN BETA-4 (HUMAN);
4781	17362	28812	4.97	2.6E+00	AF088749.1	NT	CM6-BT0281-0311169-087-h04 BT0281 Homo sapiens cDNA
5738	18362	31068	1.94	2.6E+00	6755601	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5738	18362	31069	1.94	2.6E+00	6755601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
5882	18612		2.42	2.6E+00	Y17082.1	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
7889	20188		5.98	2.6E+00	AF235502.1	NT	Mycobacterium fortuitum furA II gene
8003	20545	33447	1.08	2.6E+00	AJ132180.1	NT	Mus musculus SH2-containing inositol 5-phosphatase (Ship) gene, exons 16 through 27, and complete cds
8003	20545	33448	1.08	2.6E+00	AJ132180.1	NT	faba bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-83
9578	22076	35038	3.02	2.6E+00	AL161540.2	NT	faba bean necrotic yellows virus C2-Eg gene, isolate Egyptian EV1-93
10257	22752		1.51	2.6E+00	8055183	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
10907	23426	36443	1.89	2.6E+00	AF143875.1	NT	Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA
12390	24888		2.78	2.6E+00	11419220	NT	Hantavirus Z10 segment M G1/G2 glycoprotein (Z10) gene, complete cds
1513	14105	26840	2.29	2.5E+00	AJ271844.1	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
1513	14105	26841	2.29	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
1513	14105	26841	2.29	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4

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5981	18601	31334	1.71	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5981	18601	31335	1.71	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6586	18601	31334	1.39	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6586	18601	31335	1.39	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6828	19418	32234	0.73	2.5E+00	D30052.1	NT	Vibrio cholerae cba gene and cba gene for cholera toxins, complete cds
7736	20244	33135	1.05	2.5E+00	AW949158.1	EST_HUMAN	QV4-F10005-110500-205-g07 F10005 Homo sapiens cDNA
9032	21569	34498	1.75	2.5E+00	D50307.1	NT	Rice DNA for aldolase C-1, complete cds
9768	22264	35247	0.88	2.5E+00	BE297758.1	EST_HUMAN	601175779F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531090 5'
11724	24131		1.66	2.5E+00	AF289665.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
3047	15663	28144	0.9	2.4E+00	M24282.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' end
5033	17607	30052	6.76	2.4E+00	4503352	NT	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA
6161	18774	31536	4.02	2.4E+00	P02843	SWISSPROT	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1)
8082	20824	33536	1.99	2.4E+00	P28842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8082	20824	33537	1.99	2.4E+00	P28842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8153	20694		2.33	2.4E+00	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
8885	21124		1.82	2.4E+00	AW875126.1	EST_HUMAN	RC2-PT0004-031299-011-d05 PT0004 Homo sapiens cDNA
8762	21301	34222	8.16	2.4E+00	P24091	SWISSPROT	ENDOCHITININASE B PRECURSOR (CHN-B)
9951	22446	35427	2.59	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
9951	22446	35428	2.59	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10017	22512	35504	1.82	2.4E+00	X92511.1	NT	H.sapiens CTGF gene and promoter region
10141	22636		7.38	2.4E+00	P06089	SWISSPROT	XYLULOSE KINASE (XYLUKINASE)
10225	22720	35710	1.63	2.4E+00	BE326702.1	EST_HUMAN	hr63r06.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10225	22720	35711	1.63	2.4E+00	BE326702.1	EST_HUMAN	hr63r06.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10483	22977	35986	1.27	2.4E+00	Q51481	SWISSPROT	DENITRIFICATION REGULATORY PROTEIN NIRQ
10958	23473	36498	1.69	2.4E+00	Y14078.1	NT	Bacillus subtilis chromosomal DNA, region 75 degrees: glpPKD operon and downstream
11237	23768	36828	2.27	2.4E+00	AF158652.2	NT	Frageria X ananassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds
1296	13990	28413	11.15	2.3E+00	Z49724.1	NT	G.domesticus artificial single chain antibody gene (L3)
4199	16788		1.65	2.3E+00	AJ401081.1	NT	Bos taurus partial cytb gene for cytochrome b
6000	18620		0.91	2.3E+00	N86245.1	EST_HUMAN	J7340F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7340 5' similar to
7477	19998	32864	2.54	2.3E+00	6978564	NT	PROLYLCARBOXYPEPTIDASE
7593	25120		4.81	2.3E+00	P07189	SWISSPROT	Rattus norvegicus ATPase, Ca++ transporting, ubiquitous (Atp2a3), mRNA
7756	20264	33159	1.06	2.3E+00	X60265.1	NT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
							M.mazael dnaK and dnaJ genes homologues coding for DnaK and DnaJ

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9038	21575	34505	0.53	2.3E+00	5835317	NT	Polyporus omaliipinis mitochondrion, complete genome
9097	21633	34572	1.79	2.3E+00	Q11127	SWISSPROT	ALPHA-(1,3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE)
10881	23213	36224	2	2.3E+00	Q07076	SWISSPROT	(FUCOSYLTRANSFERASE 4) (FUCT-IV)
11612	24055	37119	2.92	2.3E+00	BF541987.1	EST_HUMAN	ANNEXIN VII (SYNEXIN)
11612	24055	37120	2.92	2.3E+00	BF541987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
11950	24278	31020	7.31	2.3E+00	BE895237.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4068173 5'
4089	16685	29143	91.07	2.2E+00	AF020528.1	NT	601433673F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3818643 5'
4403	16988	29432	4.5	2.2E+00	D67071.1	NT	Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds
4403	16988	29433	4.5	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
							Rat gene for regucalcin, exon1 (non-coding exon)
5545	18177	30591	12.27	2.2E+00	O88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND- BINDING REPEATS) (LR11) (>
5545	18177	30592	12.27	2.2E+00	O88307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND- BINDING REPEATS) (LR11) (>
6016	18635	31373	0.95	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-406 CT0254 Homo sapiens cDNA
6016	18635	31374	0.95	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-406 CT0254 Homo sapiens cDNA
6212	18822	31563	9.1	2.2E+00	BE250383.1	EST_HUMAN	600843401T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2959777 3'
6495	19068	31880	4.32	2.2E+00	Q00335	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN MJ-2
6709	19303	32107	3.04	2.2E+00	P51459	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
7037	18057		3.58	2.2E+00	AA594574.1	EST_HUMAN	ri95b02.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1058379 3'
7358	19884	32747	0.9	2.2E+00	AA137027.1	EST_HUMAN	zn9704.r1 Stratiotes fetal retina 937202 Homo sapiens cDNA clone IMAGE:568143 5'
7602	20115	32982	25.23	2.2E+00	AA449012.1	EST_HUMAN	zn05g10.r1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:785634 5'
8046	20588	33494	0.65	2.2E+00	BE301560.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);
8046	20588	33495	0.65	2.2E+00	BE301560.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);
9285	21791		12.17	2.2E+00	BE741678.1	EST_HUMAN	601594733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948561 5'
9498	24783		2.57	2.2E+00	Q04708	SWISSPROT	TRANSFOSON TY1 PROTEIN A
9866	22481	35443	1.96	2.2E+00	AI260373.1	EST_HUMAN	qm69503.x1 Soares placenta_8to8weeks_2NbHP80c9W Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9966	22461	35444	1.96	2.2E+00	A1290373.1	EST_HUMAN	qm69603.x1 Soares_placenta_8to8weeks_2NbhP8t9W Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10008	22503	35494	3.7	2.2E+00	BF246782.1	EST_HUMAN	601855591F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075391 5'
10353	22847	35841	2.99	2.2E+00	AF183416.1	NT	Homo sapiens ovarian granulosa cell 13.0 kDa protein hGR74 homolog mRNA, complete cds
11316	23014	36023	4.01	2.2E+00	P07911	SWISSPROT	UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
11482	23932	37003	4.23	2.2E+00	P10407	SWISSPROT	EARLY E1A 28 KD PROTEIN
595	15419	25699	6.28	2.1E+00	AF132612.2	NT	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
3648	18251		0.65	2.1E+00	AW449366.1	EST_HUMAN	UIH-BIS-akt-e-08-Q-UI.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'
6281	18889		0.85	2.1E+00	P75357	SWISSPROT	HYPOTHETICAL PROTEIN MG302 HOMOLOG
6899	19633	32471	3.38	2.1E+00	O70159	SWISSPROT	ALPHA-2HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
7110	19450	32266	5.13	2.1E+00	N29575.1	EST_HUMAN	Y08a10.s1 Soares_melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270618 3' similar to gb:M55654
8434	20974		2.27	2.1E+00	AU123630.1	EST_HUMAN	TRANSCRIPTION INITIATION FACTOR TFIID (HUMAN);
10454	22948		0.58	2.1E+00	Y10284.1	NT	H. sapiens TRAF1 gene, putative promoter region
1238	13836	26352	1.3	2.0E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1238	13836	26353	1.3	2.0E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1380	13973	26501	0.92	2.0E+00	AF204927.1	NT	Oryctolagus cuniculus Na ⁺ /K ⁺ -ATPase beta 1 subunit mRNA, complete cds
1619	14212		2.89	2.0E+00	P25582	SWISSPROT	PUTATIVE RRNA METHYLTRANSFERASE SPB1
2194	14770	27343	3.69	2.0E+00	Z78278.1	NT	R. norvegicus mRNA for collagen alpha1 type I
2194	14770	27344	3.69	2.0E+00	Z78278.1	NT	R. norvegicus mRNA for collagen alpha1 type I
4176	16767	29215	1.9	2.0E+00	AW664496.1	EST_HUMAN	h13c05.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677
4176	16767	29216	1.9	2.0E+00	AW664496.1	EST_HUMAN	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
7552	20071		0.77	2.0E+00	P07586	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
7967	20509	33415	3.56	2.0E+00	AB009676.1	NT	STRUCTURAL POLYPEPTIDE [CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE GLYCOPROTEINS E1 AND E2]
7967	20509	33416	3.56	2.0E+00	AB009676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
7967	20509	33417	3.56	2.0E+00	AB009676.1	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
8853	21392	34314	3.62	2.0E+00	F31500.1	EST_HUMAN	Escherichia coli 0157 DNA, map position at 46 min., complete cds
12295	21946	30622	7.77	2.0E+00	5834843	NT	HSPD22703 HM3 Homo sapiens cDNA clone s4000117B08
5784	18409	31124	6.89	1.9E+00	6754389	NT	Gallus gallus mitochondrion, complete genome
5784	18409	31125	6.89	1.9E+00	6754389	NT	Mus musculus inositol 1,4,5-triphosphate receptor 1 (ltp1), mRNA
6249	18858	31630	1.2	1.9E+00	BE969695.1	EST_HUMAN	Mus musculus inositol 1,4,5-triphosphate receptor 1 (ltp1), mRNA
6249	18858	31630	1.2	1.9E+00	BE969695.1	EST_HUMAN	601879036F1 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:3949881 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6760	19353		1.02	1.9E+00	AW845688.1	EST_HUMAN	MRO-CT0063-071099-002-g02 CT0063 Homo sapiens cDNA
6845	19435		2.31	1.9E+00	Q83827	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
8396	20936	33858	2.16	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8398	20936	33859	2.18	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8593	21132		2.45	1.8E+00	BF380206.1	EST_HUMAN	CM3-MT0114-010900-323-n12 MT0114 Homo sapiens cDNA
8825	21364		1.35	1.8E+00	O51781	SWISSPROT	ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD)
9548	22048	35009	0.8	1.9E+00	AA689125.1	EST_HUMAN	ab84a04.s1 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:854574 3' similar to contains Alu repetitive element; contains element L1 L1 repetitive element;
10458	22950	35959	0.52	1.9E+00	AF248269.1	NT	Homo sapiens gag-pro-pol precursor protein gene, partial cds
3128	15742	28211	1.88	1.8E+00	P21004	SWISSPROT	PROTEIN B8 PRECURSOR
3154	15768	28234	2.42	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (claA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3154	15768	28235	2.42	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (claA) and ATP synthase epsilon subunit (atpE) genes, complete cds
6027	18648		2.02	1.8E+00	P18502	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
6253	18862	31634	2.02	1.8E+00	BF311899.1	EST_HUMAN	601897854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127384 5'
6532	19132		1.53	1.8E+00	BF683327.1	EST_HUMAN	602139470F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4288272 5'
6838	19428	32244	1.35	1.8E+00	BF305652.1	EST_HUMAN	601893489F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139038 5'
7119	19459	32274	1.08	1.8E+00	P21249	SWISSPROT	MAJOR ANTIGEN
8060	20602	33512	0.81	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8060	20602	33513	0.81	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8788	21327	34252	2.12	1.8E+00	O43281	SWISSPROT	EMBRYONAL FN-ASSOCIATED SUBSTRATE (HEFS)
9102	21638	34577	0.83	1.8E+00	R31042.1	EST_HUMAN	yH72c08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135278 5'
9186	21703	34845	0.8	1.8E+00	AW880004.1	EST_HUMAN	QV0-OT0030-070300-149-a03 OT0030 Homo sapiens cDNA
9763	22261	35244	0.87	1.8E+00	P27050	SWISSPROT	CHITINASE D PRECURSOR
10183	22878		3.78	1.8E+00	AF111849.1	NT	Homo sapiens PRO0530 mRNA, complete cds
10447	22841		0.85	1.8E+00	P44325	SWISSPROT	CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE) (CDA)
12075	24815		6.85	1.8E+00	AF314254.1	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
12163	24403		4.06	1.8E+00	9506404	NT	Rattus norvegicus Actin-related protein complex 1b (Arpc1b), mRNA
12476	24815	30780	1.38	1.8E+00	BF212412.1	EST_HUMAN	601813714F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048251 5'

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1147	13750	26259	2.08	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE)(SUCROSE 6-FRUCTOSYL TRANSFERASE)
2311	14883	27458	2.37	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2411	14979	27554	1.29	1.7E+00	AI141067.1	EST_HUMAN	ox43h05.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'
4558	17141	26589	0.74	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE)(SUCROSE 6-FRUCTOSYL TRANSFERASE)
5787	18422	31137	1.65	1.7E+00	BE063546.1	EST_HUMAN	GM0-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA
5797	18422	31138	1.65	1.7E+00	BE063546.1	EST_HUMAN	GM0-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA
6168	18780	31545	3.35	1.7E+00	Q817R8	SWISSPROT	COUP TRANSCRIPTION FACTOR 1(COUP-TF1)(COUP-TF1)
7270	19798	32654	1.33	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7270	19798	32655	1.33	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7306	18834	32693	1.63	1.7E+00	P20393	SWISSPROT	ORPHAN NUCLEAR RECEPTOR NR1D1 (V-ERBA RELATED PROTEIN EAR-1)(REV-ERBA-ALPHA)
7796	20339	33247	0.86	1.7E+00	AF021335.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 2 and gamma 4 gene clusters
7978	20518	33425	1.34	1.7E+00	8755715	NT	Mus musculus T cell acute lymphocytic leukemia 1 (Tal1), mRNA
8006	20548	33452	0.57	1.7E+00	BF530630.1	EST_HUMAN	602071917F1 NCI_CGAP_Bim67 Homo sapiens cDNA clone IMAGE:4214669 5'
8478	21018	33933	0.61	1.7E+00	AF245513.1	NT	Hippoglossus hippoglossus interferon inducible Mx protein (Mx) mRNA, complete cds
8562	21101	34098	2.08	1.7E+00	BF308000.1	EST_HUMAN	601894255F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084 5'
8638	21177	34097	0.49	1.7E+00	X89063.1	NT	M.musculus Ank-1 mRNA for erythroid ankyrin
9078	24792	34545	2.25	1.7E+00	O60479	SWISSPROT	HOMEBOX PROTEIN DLX-3
9076	24792	34546	2.25	1.7E+00	O60479	SWISSPROT	HOMEBOX PROTEIN DLX-3
9524	22024	36885	1.65	1.7E+00	AF161380.1	NT	Homo sapiens HSPC282 mRNA, partial cds
11467	23917	36885	2.16	1.7E+00	W22424.1	EST_HUMAN	67B7 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional
12030	24320	30993	1.52	1.7E+00	AI678443.1	EST_HUMAN	tu82d07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2257549 3' similar to contains MSR1.1f1
12558	24659	30873	1.79	1.7E+00	AI198573.1	EST_HUMAN	MSR1 repetitive element;
2078	14658	27229	21.82	1.6E+00	AF199339.1	NT	qf50b01.x1 Soares_tests_NHT Homo sapiens cDNA clone IMAGE:1753417 3' similar to contains L1.11 L1 repetitive element;
2087	14668	27238	4.3	1.6E+00	AF077374.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2093	14673	27243	1.04	1.6E+00	Y11344.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2323	14894		1.13	1.6E+00	X98373.1	NT	Mus musculus ST6GalNAcII gene, exon 2
2988	15804	28084	1.5	1.6E+00	W59426.1	EST_HUMAN	B.napus gene encoding endo-polygalacturonase
4104	16898		7.23	1.6E+00	BF570077.1	EST_HUMAN	zid2501.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341689 5' similar to gb:D29805 N-ACETYLLACTOSAMINE SYNTHASE (HUMAN);
						EST_HUMAN	602186095T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310501 3'

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Table 4

Single Exon Probes Expressed in Fatal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4444	17030	29470	1.11	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA8) mRNA, complete cds
4444	17030	29471	1.11	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA8) mRNA, complete cds
5145	17715	30145	0.6	1.6E+00	AF075394.1	NT	Uroteuthis chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
5145	17715	30146	0.6	1.6E+00	AF075394.1	NT	Uroteuthis chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
5243	17807	30228	2.2	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
5243	17807	30229	2.2	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
5993	18613	31347	1.95	1.6E+00	L04808.1	NT	Brachydanio rerio MHC class II DA-beta-2*01 gene, 3' end
6072	18689	31434	0.92	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (Tgase1) gene, promoter region
6596	19193	31998	0.93	1.6E+00	BF360703.1	EST_HUMAN	IL2-UT0073-060900-145-E02 UT0073 Homo sapiens cDNA
6811	19402	32218	1.07	1.6E+00	AW294881.1	EST_HUMAN	U1-H-PI2-ant-b-04-0-U1.s1 NCL_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727511 3'
7293	19921	32680	2.32	1.6E+00	BE697267.1	EST_HUMAN	RCO-CT0415-200700-032-g10 CT0415 Homo sapiens cDNA
7973	20515		1.09	1.6E+00	Q46378	SWISSPROT	VIRULENCE FACTOR MYIN HOMOLOG
8320	20961	33786	3.24	1.6E+00	AJ287131.1	NT	Mus musculus SIL MAP 17, CYP a, SCL & CYP b genes
8831	21370	34284	0.95	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0871 (PRO0871), mRNA
8831	21370	34285	0.95	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0871 (PRO0871), mRNA
8381	24780	33221	3.16	1.6E+00	X52048.1	NT	Mus musculus COL3A1 gene for collagen alpha-1
8381	24790	33222	3.16	1.6E+00	X52046.1	NT	Mus musculus COL3A1 gene for collagen alpha-1
8849	22148	35119	1.34	1.6E+00	T41290.1	EST_HUMAN	ph866_19/1 TV Outward Alu-pri-med hmcDNA library Homo sapiens cDNA clone ph866_19/1TV
10052	22547	35541	0.52	1.6E+00	AF121361.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase Ial (IAL), and zinc finger protein (DNZ1) genes, complete cds
10088	22583	35575	0.92	1.6E+00	AW835644.1	EST_HUMAN	QV4-LT0016-090200-100-407 LT0016 Homo sapiens cDNA
10088	22583	35578	0.92	1.6E+00	AW835644.1	EST_HUMAN	QV4-LT0016-090200-100-407 LT0016 Homo sapiens cDNA
10246	22741	35731	0.49	1.6E+00	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
10650	23182	36196	1.59	1.6E+00	PS4817	SWISSPROT	CAPSID PROTEIN P40 (CONTAINS: ASSEMBLIN (PROTEASE); CAPSID ASSEMBLY PROTEIN)
10686	23216	36228	1.56	1.6E+00	PS4817	SWISSPROT	CAPSID PROTEIN P40 (CONTAINS: ASSEMBLIN (PROTEASE); CAPSID ASSEMBLY PROTEIN)
10723	18689	31434	6.41	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (Tgase1) gene, promoter region
11552	24000	37072	2.92	1.6E+00	AF104313.1	NT	Homo sapiens unknown mRNA
35	12714	25173	4.02	1.5E+00	U59449.1	NT	Rattus norvegicus Jun dimerization protein 2 (Jdp-2) mRNA, complete cds
252	12912	25396	2.17	1.5E+00	AE002201.2	NT	Chlamydia pneumoniae AR39, section 32 of 94 of the complete genome
649	13272		1.98	1.5E+00	6752861	NT	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metagardin) (Adam15), mRNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1960	14544	27101	2.55	1.5E+00	AF275265.1	NT	Mus musculus receptor protein tyrosine phosphatase-rho (Ptptr) gene, exons 10 and 11 and partial cds
2454	15021	27592	2.13	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
2556	15120	27690	1.83	1.5E+00	6878350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA
3172	15021	27592	1.54	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3421	18029	28510	0.7	1.5E+00	AE001945.1	NT	Deinococcus radiodurans R1 section 82 of 228 of the complete chromosome 1
5903	18525	31250	0.94	1.5E+00	AI655301.1	EST_HUMAN	ht2f10.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:O00237 O00237 HKF-1.1
5903	18525	31251	0.94	1.5E+00	AI655301.1	EST_HUMAN	ht2f10.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:O00237 O00237 HKF-1.1
6538	19137	31930	2.68	1.5E+00	R17879.1	EST_HUMAN	y010e02.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31693 5'
7182	19714		1.37	1.5E+00	BE785356.1	EST_HUMAN	601478745F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881555 5'
7214	19745	32599	20.84	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7214	19745	32600	20.84	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7383	19909	32774	1.02	1.5E+00	AA889259.1	EST_HUMAN	ak28f10.s1 Soares testis NIH-T Homo sapiens cDNA clone IMAGE:1407115 3'
8085	20607	33519	0.85	1.5E+00	BE887448.1	EST_HUMAN	601509886F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911181 5'
8578	21117	34037	1.1	1.5E+00	K02138.1	NT	Mouse germline IgM chain gene, mu-delta region
8946	21484		0.53	1.5E+00	AB038516.1	NT	Homo sapiens hGP1b alpha gene for platelet glycoprotein Ib alpha, complete cds
9061	21598	34528	0.54	1.5E+00	BF217818.1	EST_HUMAN	601882662F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095135 5'
9404	21913	34862	0.9	1.5E+00	R81928.1	EST_HUMAN	y03h01.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147697 5'
9553	22053	35016	1.12	1.5E+00	AW375697.1	EST_HUMAN	QV3-CT0192-261099-008-d09 CT0192 Homo sapiens cDNA
9774	22272	35257	5.97	1.5E+00	BF378754.1	EST_HUMAN	RCO-TN0078-150900-034-q05 TN0078 Homo sapiens cDNA
9865	22460		1.47	1.5E+00	BF337844.1	EST_HUMAN	602035771F1 NCL_CGAP_Bim84 Homo sapiens cDNA clone IMAGE:4183865 5'
10098	22593	35585	2.95	1.5E+00	AA017689.1	EST_HUMAN	ze38g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
10098	22593	35586	2.95	1.5E+00	AA017689.1	EST_HUMAN	ze38g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:361306 5'
11277	23730	36785	4.1	1.5E+00	AL131497.1	EST_HUMAN	DKFZp547P243.s1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547P243 3'
11416	23867		9.57	1.5E+00	X07380.1	NT	Maize mitochondrial rRNA-Ser gene and rRNA-Phe pseudogene
12022	25010	30615	1.59	1.5E+00	D63480.1	NT	Human mRNA for KIAA0146 gene, partial cds
12255	24465		4.99	1.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
32	12711	25169	1.8	1.4E+00	7681685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
32	12711	25170	1.8	1.4E+00	7681685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1774	14364	26909	1.32	1.4E+00	H19859.1	EST_HUMAN	yn57e03.r1 Soares adult brain N2b5HB53Y Homo sapiens cDNA clone IMAGE:172540 5'
2316	14888		0.98	1.4E+00	AF053357.1	NT	Helicobacter pylori glutamine synthetase (glhA) gene, complete cds
2372	14942		7.8	1.4E+00	U67922.1	NT	Ovis aries prion protein gene, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptpr
2693	15250	27820	1.45	1.4E+00	X74463.1	NT	Human papillomavirus type 7 genomic DNA
2802	15354	27922	2.79	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2802	15354	27923	2.79	1.4E+00	AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
3376	15985		0.68	1.4E+00	5453733	NT	Human sapiens Mad4 homolog (MAD4) mRNA
4342	16929	28369	1.14	1.4E+00	AW900455.1	EST_HUMAN	CMO-NN1005-140300-286-H08 NN1005 Homo sapiens cDNA
4342	16929	28370	1.14	1.4E+00	AW900455.1	EST_HUMAN	CMO-NN1005-140300-286-H08 NN1005 Homo sapiens cDNA
4885	17287		1.78	1.4E+00	BF681547.1	EST_HUMAN	602156887F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297556 5'
5575	18206	30657	1.76	1.4E+00	AW054976.1	EST_HUMAN	w145p07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510480 3'
5719	18345		5.04	1.4E+00	AB032983.1	NT	Homo sapiens mRNA for KIAA1157 protein, partial cds
6425	18028	31811	2.73	1.4E+00	Q13472	SWISSPROT	DNA TOPOISOMERASE III ALPHA
6437	25116		4.4	1.4E+00	AB020712.1	NT	Homo sapiens mRNA for KIAA0905 protein, complete cds
6544	19143	31936	2.32	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
6544	19143	31937	2.32	1.4E+00	Q92777	SWISSPROT	Mus musculus WW domain binding protein 11 (Wbp11-pending), mRNA
6583	19181	31881	0.67	1.4E+00	11096333	NT	CM3-NN0006-300300-132-b12 NN0006 Homo sapiens cDNA
6911	19570	32398	0.77	1.4E+00	AW893057.1	EST_HUMAN	Homo sapiens cavedin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7330	19857	32720	2.31	1.4E+00	AJ133269.1	NT	he23f05.x1 NCI_CGAP_OML1 Homo sapiens cDNA clone IMAGE:2919873 3' similar to contains Alu repetitive element;
7343	19870	32735	1.1	1.4E+00	AW467760.1	EST_HUMAN	GLUCOAMYLASE PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
8277	20818		0.68	1.4E+00	P07683	SWISSPROT	Homo sapiens Xq pseudautosomal region, segment 1/2
8729	21268		4.01	1.4E+00	AJ271735.1	NT	yq33f12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34345 5'
9023	21560	34487	2.13	1.4E+00	R20459.1	EST_HUMAN	RC1-BT0313-301289-012-05 BT0313 Homo sapiens cDNA
9125	21660	34603	3.72	1.4E+00	BE064967.1	EST_HUMAN	Sceloporus undulatus ornithine transcarbamylase (OTC) mRNA, complete cds
9158	21693	34637	0.58	1.4E+00	AF134844.1	NT	602133135F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288137 5'
10109	22604	35594	0.77	1.4E+00	BF575545.1	EST_HUMAN	IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA
10150	22645	35637	0.67	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA
10150	22645	35638	0.67	1.4E+00	BE145374.1	EST_HUMAN	Pandorina colemaniae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10418	22912	35912	1.11	1.4E+00	D63441.1	NT	Pandorina colemaniae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10418	22912	35913	1.11	1.4E+00	D63441.1	NT	z33609.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:685512 5' similar to contains element
10948	23463	36485	2.16	1.4E+00	AA195528.1	EST_HUMAN	MER22 repetitive element;

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11104	23614	36654	6.28	1.4E+00	AB006682.1	NT	Homo sapiens APECE2 mRNA for AIRE-1, complete cds
11283	23736	36791	3.92	1.4E+00	BE962107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11283	23736	36792	3.92	1.4E+00	BE962107.2	EST_HUMAN	601655184R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845805 3'
11304	23797	36855	3.19	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. retri guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
11304	23797	36856	3.19	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. retri guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
11865	24935		2.43	1.4E+00	AL161500.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
12267	25108		2.38	1.4E+00	11548836	NT	Homo sapiens cutaneous T-cell lymphoma tumor antigen se70-2 (SE70-2), mRNA
596	13225		1.38	1.3E+00	Z73840.1	NT	M.mucedo gene encoding 4-Dihydropyrimidin-bisphosphate dehydrogenase
935	13548	26065	2.33	1.3E+00	AJ271192.1	NT	Cantharellus sp. partial 25S rRNA gene, isolate Tibet
1168	13770		22.19	1.3E+00	Y19213.1	NT	Homo sapiens putative psithbA pseudogene for hair keratin, exons 2 to 7
1340	13935	28456	13.67	1.3E+00	4507898	NT	Homo sapiens zinc finger protein 157 (ZF157) mRNA
1340	13935	28457	13.67	1.3E+00	4507898	NT	Homo sapiens zinc finger protein 157 (ZF157) mRNA
1400	13994		1.05	1.3E+00	U61730.2	NT	Ccix lacryme-jobi dihydropyrimidine synthase (dapA) gene, complete cds
1653	14245		2.35	1.3E+00	AE002338.2	NT	Chlamydia muridarum, section 66 of 85 of the complete genome
2285	14859		1.1	1.3E+00	AB030447.1	NT	Cyprinus carpio MRPs and MASPs genes for mannose-binding lectin-associated serine protease (MASP) and MASP-related protein, complete cds
2586	15149		0.97	1.3E+00	BE966735.2	EST_HUMAN	601661233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915945 3'
2868	15581	28060	0.66	1.3E+00	6755621	NT	Mus musculus alpha-spectrin 1, erythroid (Spn1), mRNA
3657	16260	28732	0.91	1.3E+00	AF016494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c
4713	15581	28060	1.31	1.3E+00	6755621	NT	Mus musculus alpha-spectrin 1, erythroid (Spn1), mRNA
5184	17749	30178	0.92	1.3E+00	AJ252087.1	NT	Plasmodium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1
5184	17749	30179	0.92	1.3E+00	AJ252087.1	NT	Plasmodium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1
5705	18331	30835	1.06	1.3E+00	P19732	SWISSPROT	PHENOL HYDROXYLASE P3 PROTEIN (PHENOL 2-MONOOXYGENASE P3 COMPONENT)
6169	18781	31546	7.47	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0289-291189-004-08 CT0289 Homo sapiens cDNA
6169	18781	31547	7.47	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0289-291189-004-08 CT0289 Homo sapiens cDNA
6549	19147	31943	1.24	1.3E+00	M33466.1	NT	D.melanogaster no-on-transient A gene product, complete cds
6847	19437		0.71	1.3E+00	Q00156	SWISSPROT	HYPOTHETICAL GENE 64 PROTEIN
6926	19585	32415	0.85	1.3E+00	M13918.2	NT	Homo sapiens fibronectin receptor alpha-subunit precursor (ITGA5) mRNA, partial cds
7033	19567	32394	1.01	1.3E+00	BE538819.1	EST_HUMAN	601061420F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447965 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7157	19689	32533	0.79	1.3E+00	BE243571.1	EST_HUMAN	TCBAP1D0959 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project=TCBA Homo sapiens cDNA clone TCBAP0959
7481	20003	32868	3.97	1.3E+00	P24540	SWISSPROT	ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYMES A AND B (ACYLPHOSPHATE PHOSPHOHYDROLASE)
8239	20780	33701	2.06	1.3E+00	AJ009912.1	NT	Sus scrofa pig gene
8384	20924	33944	2.54	1.3E+00	BE963379.2	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868195 3'
8498	21035	33966	0.99	1.3E+00	BE974280.1	EST_HUMAN	601680250R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950532 3'
8644	21183		1.57	1.3E+00	9910247	NT	Homo sapiens GL004 protein (GL004), mRNA
8725	21284	34184	0.88	1.3E+00	A1927628.1	EST_HUMAN	yc685a07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
9073	21610	34540	0.48	1.3E+00	H42881.1	EST_HUMAN	yc68c03.s1 Soares breast 3NBHBst Homo sapiens cDNA clone IMAGE:183076 3'
9073	21610	34541	0.48	1.3E+00	H42881.1	EST_HUMAN	yc68c03.s1 Soares breast 3NBHBst Homo sapiens cDNA clone IMAGE:183076 3'
9434	21960		4.54	1.3E+00	AF042084.1	NT	Homo sapiens heparan glucosaminyl N-deacetylase/N-sulfotransferase-2 gene, complete cds
9443	21969	34917	2.12	1.3E+00	X72019.1	NT	S.alba pfr-1 mRNA for photolyase
9443	21969	34918	2.12	1.3E+00	X72019.1	NT	S.alba pfr-1 mRNA for photolyase
9542	22042	35003	1.1	1.3E+00	AF059250.1	NT	Homo sapiens lipoxigenase (ALOX12B) mRNA, complete cds
9588	22088	35052	1.62	1.3E+00	O00754	SWISSPROT	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE)(LAMMAN)
9665	22164	35137	1.21	1.3E+00	A1927628.1	EST_HUMAN	yc685a07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
9740	22238	35218	0.83	1.3E+00	AJ223962.1	NT	Lactobacillus lactis cremoris NCDO-inv1 chromosomal inversion junction DNA
9740	22238	35219	0.83	1.3E+00	AJ223962.1	NT	Lactobacillus lactis cremoris NCDO-inv1 chromosomal inversion junction DNA
9780	22278	35263	3.85	1.3E+00	BE963379.2	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868195 3'
10114	22609	35600	1.25	1.3E+00	AE004392.1	NT	Vibrio cholerae chromosome II, section 49 of 83 of the complete chromosome
10130	22625	35615	2.41	1.3E+00	M29853.1	NT	Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds
10476	22970		0.65	1.3E+00	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
10504	22988		0.52	1.3E+00	8823637	NT	Homo sapiens hypothetical protein FLJ20707 (FLJ20707), mRNA
10507	23001	36008	0.48	1.3E+00	H42881.1	EST_HUMAN	yc68c03.s1 Soares breast 3NBHBst Homo sapiens cDNA clone IMAGE:183076 3'
10507	23001	36009	0.48	1.3E+00	H42881.1	EST_HUMAN	yc68c03.s1 Soares breast 3NBHBst Homo sapiens cDNA clone IMAGE:183076 3'
10573	23108		4.66	1.3E+00	Q14117	SWISSPROT	DIHYDROPYRIMIDINASE (DHPASE) (HYDANTOINASE) (DHP)
10765	23309	36316	2.3	1.3E+00	P25289	SWISSPROT	MRNA 3'-END PROCESSING PROTEIN RNA15
10807	23330	36342	2.17	1.3E+00	Z18882.2	NT	Mus musculus desmin gene
11215	23718		1.87	1.3E+00	AW274791.1	EST_HUMAN	xc09803.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2739888 3'
11414	23865	36928	3.09	1.3E+00	D42042.1	NT	Human mRNA for KIAA0085 gene, partial cds
11488	23937	37007	3.09	1.3E+00	Z98682.1	NT	Bacillus subtilis genomic DNA 23.9k fragment
12011	24312		3.63	1.3E+00	AF187873.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12192	24423	30949	3.47	1.3E+00	BF348043.1	EST_HUMAN	602023185F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4158452 5'
12204	24826		1.76	1.3E+00	P33484	SWISSPROT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
12303	24900		2.08	1.3E+00	AF187035.1	NT	Sturtia liliium cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
12673	24904		1.25	1.3E+00	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
878	13302	25784	9.75	1.2E+00	AA678246.1	EST_HUMAN	Z122d08.s1 Soares_fetal_liver_spleen_1NPLS_S1 Homo sapiens cDNA clone IMAGE:431535 3'
858	13472	25883	1.04	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
856	13472	25984	1.04	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
858	13472	25985	1.04	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
911	13524		1.9	1.2E+00	8824234	NT	Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA
1203	13803	26316	4.87	1.2E+00	AF060245.2	NT	Elaeis oleifera sesquiterpene synthase mRNA, complete cds
1247	13844	26361	1.3	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1247	13844	26362	1.3	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
2054	14935	27208	53.59	1.2E+00	AF140831.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
2417	14985	27559	1.53	1.2E+00	AF156495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
3144	15758	28224	1.16	1.2E+00	AB020881.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3201	15813	28287	7.17	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3201	15813	28288	7.17	1.2E+00	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3325	15835		3.43	1.2E+00	P54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3399	16007	28489	0.57	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
3774	16374	28838	8.66	1.2E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
4058	16655	28121	1.87	1.2E+00	BF373570.1	EST_HUMAN	MR0-FT0175-050900-203-q06_1 FT0175 Homo sapiens cDNA
4386	16007	28489	1.12	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
4570	17153		2.09	1.2E+00	M87060.1	NT	Rattus rattus cardiac AE3 gene, exons 1-23
4621	17204	28653	1.08	1.2E+00	AL161509.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4659	17241	28685	1.5	1.2E+00	AF158495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4690	17272		9.41	1.2E+00	Y09200.1	NT	T. pinatum chloroplast rbcL gene, partial
4791	18008		0.77	1.2E+00	M81779.1	NT	G.gallus T-cadherin mRNA, complete cds
5629	18258	30729	1.06	1.2E+00	U20760.1	NT	Human extracellular calcium-sensing receptor mRNA, complete cds
5743	18369	31077	2.27	1.2E+00	AW813276.1	EST_HUMAN	MR3-ST0191-140200-013-q05 ST0191 Homo sapiens cDNA
6034	18653	31395	0.72	1.2E+00	AF016052.1	NT	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
6300	18908	31678	2.17	1.2E+00	X74885.1	NT	D.hydrel av1 repeat cluster DNA, fragment D
6361	18965	31743	3.98	1.2E+00	BE003113.1	EST_HUMAN	QV4-BN0090-270400-190-a03 BN0090 Homo sapiens cDNA
6433	19036	31822	1.43	1.2E+00	X89084.1	NT	C.glutamicum pla gene and ackA gene
6433	19036	31823	1.43	1.2E+00	X89084.1	NT	C.glutamicum pla gene and ackA gene

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6475	19078	31859	34.96	1.2E+00	AA759254.1	EST_HUMAN	ab84p12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1322374 3'
6629	19225	32030	2.25	1.2E+00	AW813278.1	EST_HUMAN	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
6995	19493	32314	1.18	1.2E+00	AB029010.1	NT	Homo sapiens mRNA for KIAA1087 protein, partial cds
7007	19505	32324	2.8	1.2E+00	AJ002141.1	NT	Mus musculus DSPP gene
7300	19828	32808	0.8	1.2E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region: segment 1/2
7417	24782	32808	1.59	1.2E+00	AV734585.1	EST_HUMAN	AV734585 cda Homo sapiens cDNA clone cdAAFH03 5'
7646	20158	33045	2.84	1.2E+00	X74207.1	NT	L.lactis pyrD and pyrF genes
8504	21043	33964	3.05	1.2E+00	AB033030.1	NT	Homo sapiens mRNA for KIAA1204 protein, partial cds
							ALPHA-ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (UDP-FORMING) 123 KD SUBUNIT (TREHALOSE-6-PHOSPHATE SYNTHASE) (UDP-GLUCOSE-GLUCOSEPHOSPHATE GLUCOSYLTRANSFERASE)
8597	21138	34051	0.69	1.2E+00	P39427	SWISSPROT	Homo sapiens CGI-30 protein (LOC51811), mRNA
8809	21348		0.53	1.2E+00	7706271	NT	MR2-CT0222-201099-001-407 CT0222 Homo sapiens cDNA
8955	21493	34416	2.03	1.2E+00	AW377210.1	EST_HUMAN	R.communis gene for pyrophosphate-dependent phosphofructokinase beta subunit
9319	21833	34783	2.92	1.2E+00	Z2850.1	EST_HUMAN	HUM-HM01A01 Liver HepG2 cell line. Homo sapiens cDNA clone hm01a01
9523	22023	34981	1.86	1.2E+00	D11745.1	NT	H.sapiens ENO3 gene for muscle specific endase
9844	22342	35324	3.47	1.2E+00	X58832.1	NT	Homo sapiens Klotho gene, exon 1
10229	22724		0.87	1.2E+00	AB009668.1	NT	PM0-ST0284-161196-001-d01 ST0284 Homo sapiens cDNA
11224	23755	36813	2.19	1.2E+00	AW817817.1	EST_HUMAN	PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA
11262	23760		6.84	1.2E+00	BE160761.1	EST_HUMAN	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
11331	23029	36038	3.76	1.2E+00	U50147.1	NT	Homo sapiens chromosome 21 segment HS21C003
11976	24907	30712	32.4	1.2E+00	AL163203.2	NT	Bacillus halodurans genomic DNA, section 8/14
11988	24304		2.11	1.2E+00	AP001515.1	NT	Human mRNA for KIAA0227 gene, partial cds
489	13122	25608	1.19	1.1E+00	D86980.1	NT	QV0-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
1799	14389	26934	1.48	1.1E+00	AW995393.1	EST_HUMAN	W heat yellow mosaic virus RNA1 270 kDa precursor protein gene, complete cds
2617	15179	27746	1.09	1.1E+00	AF067124.1	NT	Homo sapiens chromosome 21 segment HS21C013
3373	15981	28458	9.32	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3373	15981	28459	9.32	1.1E+00	AL163213.2	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3533	16138	28620	0.84	1.1E+00	8922841	NT	SW:PS31_HUMAN Q12888 P53-BINDING PROTEIN 53BP1 ;
3639	16242	28718	1.06	1.1E+00	AI808360.1	EST_HUMAN	Xyella fastidiosa, section 32 of 229 of the complete genome
3781	16381	28945	1.41	1.1E+00	AE003888.1	NT	Xyella fastidiosa, section 32 of 229 of the complete genome
3781	16381	28848	1.41	1.1E+00	AE003888.1	NT	H.parahaemolyticus hphIM(A), hphIM(C), hphIR and menB genes
3899	16488		0.61	1.1E+00	X85374.1	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
4016	16614	28087	0.67	1.1E+00	8922841	NT	

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4093	16688	29145	0.65	1.1E+00	0755205	NT	Mus musculus probasome (prosome, macroprotein) subunit, beta type 7 (Pamb7), mRNA
4295	16881		7.81	1.1E+00	5835331	NT	R.unicornis complete mitochondrial genome
5131	17703	30137	3.54	1.1E+00	U18488.1	NT	African swine fever virus, complete genome
5132	17704	30138	0.86	1.1E+00	AJ271740.1	NT	Drosophila melanogaster D-Titin gene, exons 1-37
5201	17766	30180					Emricella nidulans sterigmatocystin biosynthetic gene cluster: (stcA), (stcB), (stcC), (stcE), (stcF), (stcI), (stcJ), (stcK), (stcL), (stcM), (stcN), (stcO), (stcP), (stcQ), (stcR), (stcS), (stcT), (stcU), (stcV) and (stcW) genes, complete cds
5230	17794	30213	0.96	1.1E+00	U34740.1	NT	E.faecalis pbp5 gene
5409	17866		1.04	1.1E+00	AE003869.1	NT	Xylella fastidiosa, section 15 of 229 of the complete genome
5510	18143	30555	1.52	1.1E+00	6978530	NT	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA
5798	18423	31139	19.98	1.1E+00	BE960184.1	EST_HUMAN	601652776R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3825835 3'
5815	18439	31161	3.23	1.1E+00	AI138582.1	EST_HUMAN	qd85c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738280 3'
6242	18851	31621	1.25	1.1E+00	11418738	NT	Homo sapiens solute carrier family 8 (neurotransmitter transporter), member 14 (SLC8A14), mRNA
6420	19023	31807	0.71	1.1E+00	AF197881.1	NT	Macrogartia pulchra cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
6539	19138	31931	0.71	1.1E+00	R06037.1	EST_HUMAN	ye89e03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124924 5'
6817	19408	32225	0.7	1.1E+00	AJ404004.1	NT	Mus musculus mRNA for ER protein 58 (EP58 gene)
7338	19865	32729	0.78	1.1E+00	X55981.1	NT	Maize mRNA for endase (2-phospho-D-glycerate hydrolase)
7501	20023	32886	2.08	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7501	20023	32887	2.08	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7521	20041	32910	9.72	1.1E+00	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7580	24787	32973	0.99	1.1E+00	11987960	NT	Mus musculus eilant mating type information regulation 2, (S. cerevisiae, homolog)-like (Sir2l), mRNA
8074	20616	33530	2.8	1.1E+00	BF693998.1	EST_HUMAN	602082582F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4248628 5'
8163	20704	33620	0.75	1.1E+00	AJ478339.1	EST_HUMAN	hm39h11.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160549 3'
8672	21211	34130	0.75	1.1E+00	AB003088.1	NT	Acetabularia calliculus mitochondrial COX-like gene
8749	21288	34208	0.78	1.1E+00	S80750.1	NT	VH=ant-cytomegalovirus glycoprotein B antibody 4D4 heavy chain variable region [human, mRNA Partial, 375 nt]
8958	20297		0.68	1.1E+00	BE384876.1	EST_HUMAN	601276278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617418 5'
9546	22046	35007	0.68	1.1E+00	AJ245772.1	NT	Mus musculus mRNA for stretch responsive muscle (X-chromosome) protein (Srmx gene)
9599	22099		0.81	1.1E+00	Y12227.1	NT	Arabidopsis thaliana DNA, 24 kb surrounding PFL locus
9887	22186	35160	0.84	1.1E+00	L78301.1	NT	Yersinia pseudotuberculosis psaE, psaF, adhesin (psaA), chaperone (psaB), and usher (psaC) genes, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9747	22245	35228	1.59	1.1E+00	AB023151.1	NT	Homo sapiens mRNA for KIAA0834 protein, partial cds
9850	22348	35330	4.82	1.1E+00	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9909	22409	35381	19.39	1.1E+00	8754027	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
10395	22889	35883	1	1.1E+00	P73789	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10530	23087	36079	2.93	1.1E+00	11067384	NT	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
10586	23121		4.06	1.1E+00	AF068942.1	NT	Klebsoridium fluitans cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
10976	18026		5.26	1.1E+00	8922973	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
10983	23497	36526	3.76	1.1E+00	AF012862.1	NT	Petrosselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
10983	23497	36527	3.76	1.1E+00	AF012862.1	NT	Petrosselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11234	23765	36822	6.02	1.1E+00	AI809686.1	EST_HUMAN	w76e11.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:2361548 3'
11946	24275		1.82	1.1E+00	P07868	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
12051	24335	30897	2.25	1.1E+00	AF216898.1	NT	Taenia solium immunogenic protein T s76 mRNA, partial cds
12184	24803		1.84	1.1E+00	AF234189.1	NT	Dichostelium discoideum isopentenyl pyrophosphate isomerase (DipI) mRNA, complete cds
103	12779		3.22	1.0E+00	U23608.1	NT	Xenopus laevis rhodopsin gene, complete cds
118	12789	25271	3.48	1.0E+00	D88425.1	NT	Cavia cobaya mRNA for acetylcholine kinase, complete cds
443	13076		2.14	1.0E+00	AB021884.1	NT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
602	13231	25704	1.53	1.0E+00	AJ251680.1	NT	Giardia tigrina mRNA for homeodomain transcription factor (so gene)
705	13326	25813	7.12	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
707	13328		0.89	1.0E+00	AF125984.1	NT	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds
1426	15441		1.73	1.0E+00	X80416.1	NT	V. carteri Algal-CAM mRNA
1784	14384	26929	0.91	1.0E+00	AB008531.1	NT	Plautia stali Intesline virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds
2526	15090	27662	1.2	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2526	15090	27663	1.2	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2900	15517	27968	4.47	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2900	15517	27987	4.47	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2964	15610		0.83	1.0E+00	O14226	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN C6F12.08C IN CHROMOSOME I
3232	15844	26324	0.91	1.0E+00	AA828453.1	EST_HUMAN	af28g08.s1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to WP:CA2D8.3 CE04204 ; contains element MER22 MER22 repetitive element ;

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3659	12779		0.78	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
3744	16345	28813	1.55	1.0E+00	AJ223816.1	NT	Agaricus bisporus mRNA for tyrosinase
4144	16736	29189	1.5	1.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4362	16949		0.64	1.0E+00	8922245	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
5165	17734		17.2	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
5339	17900		0.6	1.0E+00	AF200817.1	NT	Pilot whale morbillivirus phosphoprotein (P) gene, partial cds
5432	18010	30394	1	1.0E+00	AB039022.1	NT	Oncorhynchus mykiss st1 mRNA for rhamnose binding lectin STL1, complete cds
5488	18120	30527	2.56	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
6013	18633	31368	4.54	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6013	18633	31369	4.54	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6111	18727	31480	1.22	1.0E+00	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA1 FCA contig fragment No. 6
6263	18871	31641	4.41	1.0E+00	P04501	SWISSPROT	FIBER PROTEIN
6269	18877	31645	1.56	1.0E+00	AW452782.1	EST_HUMAN	UHH-B13-alk-d09-0-UL.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068969 3'
6615	19212	32018	1.79	1.0E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
6682	19258	32082	0.83	1.0E+00	AF104689.1	NT	Homo sapiens cell cycle protein (PA2G4) gene, exons 2 through 5
6742	19336		1.5	1.0E+00	P46506	SWISSPROT	SRB-11 PROTEIN
6874	19608	32442	1.27	1.0E+00	Y11204.1	NT	V. carteri gene encoding volvoxopsin
7192	19724	32573	1.22	1.0E+00	S52770.1	NT	insulin-like growth factor-binding protein 4 [cattle, pulmonary artery endothelial cells, mRNA, 2028 nt]
7493	20016		8.58	1.0E+00	P20273	SWISSPROT	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM)
7697	20206	33083	1.38	1.0E+00	AF192531.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
7710	20219	33107	7.92	1.0E+00	AA775191.1	EST_HUMAN	ac79b05.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:868791 3'
7902	20444	33349	1.49	1.0E+00	BE868287.1	EST_HUMAN	801443950F1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3848005 5'
7902	20444	33350	1.49	1.0E+00	BE868287.1	EST_HUMAN	801443950F1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3848005 5'
8084	17734		1.28	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
8291	20832	33753	2.1	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE]

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8291	20932	33754	2.1	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
8413	20953		0.85	1.0E+00	P51784	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 11) (DEUBIQUITINATING ENZYME 11)
8447	20987	33902	0.48	1.0E+00	Q9Y5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBP-M)
8447	20987	33903	0.48	1.0E+00	Q9Y5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBP-M)
8475	24791		2.17	1.0E+00	BE147331.1	EST_HUMAN	RC1-HT0229-181098-011-608 HT0229 Homo sapiens cDNA
8513	21052	33974	1.06	1.0E+00	U42720.2	NT	Simian immunodeficiency virus Gag protein (gag) gene, complete cds; Pol protein (pol) gene, partial cds; and Vif protein (vif), Vpr protein (vpr), Tat protein (tat), Rev protein (rev), Vpu protein (vpu), Env protein (env), and Nef protein (nef) genes; >
8659	21188	34116	1.07	1.0E+00	M38427.1	NT	Human immunodeficiency virus type 1 (HIV-1), isolate SF33.
9195	21712	34655	2.05	1.0E+00	BE907592.1	EST_HUMAN	601497581 F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899421 5'
9402	21911	34860	1.34	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA
9402	21911	34861	1.34	1.0E+00	6753429	NT	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA
9528	22028	34987	2.06	1.0E+00	AV089554.1	EST_HUMAN	AV689554 GKC Homo sapiens cDNA clone GKCYA11 5'
9534	22034	34993	1.33	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xZPC) mRNA, complete cds
9534	22034	34994	1.33	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xZPC) mRNA, complete cds
9767	22265	35248	0.5	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
9767	22265	35249	0.5	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
10021	22516	35510	0.62	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHCBBF) mRNA
10021	22516	35511	0.62	1.0E+00	5174562	NT	Homo sapiens MHC binding factor, beta (MHCBBF) mRNA
10106	22800	35592	0.75	1.0E+00	A077920.1	EST_HUMAN	0715d07.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1665901 3'
10230	22725	35716	4.17	1.0E+00	AV758925.1	EST_HUMAN	AV758925 BM Homo sapiens cDNA clone BMFAW04 5'
10372	22896	35859	19.78	1.0E+00	AA004682.1	EST_HUMAN	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428908 5'
10372	22896	35860	19.78	1.0E+00	AA004682.1	EST_HUMAN	zh94a02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428908 5'
10404	22898	35893	0.93	1.0E+00	L11910.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
10853	23374	36393	1.87	1.0E+00	S00825.1	NT	PBR1=proline-rich protein (intron 3) [human, Genomic, 898 nt]
11587	18120	30527	1.57	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
11837	24201		4.85	1.0E+00	P15306	SWISSPROT	THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12171	24410		3.08	1.0E+00	AW978184.1	EST_HUMAN	EST388283 IMAGE resequences, MAGN Homo sapiens cDNA
1616	14209	26742	0.97	9.9E-01	AF245455.1	NT	Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds
1616	14209	26743	0.97	9.9E-01	AF245455.1	NT	Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds
2664	15222	27794	1.17	9.9E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3665	16267		0.94	9.9E-01	AF174585.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
5816	18440	31162	14.59	9.9E-01	P49657	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN
6029	18848	31389	0.83	9.9E-01	Q09832	SWISSPROT	PROBABLE OXIDOREDUCTASE ZK1290.5 IN CHROMOSOME II
9185	21702		1.39	9.9E-01	U65667.1	NT	Lycopodium obscurum putative Mit copy 1 nematode-resistance gene
9474	21873		2.61	9.9E-01	Q28642	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
10593	23128	36142	1.68	9.9E-01	AJ005029.1	NT	Danio rerio mRNA for Eph-like receptor tyrosine kinase rtk8
549	13180	25658	1.77	9.8E-01	P22567	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS) (NAGS)
2336	14907		0.89	9.8E-01	AJ003108.1	NT	Caillithrix jacchus UBE1 gene derived retroposon on the Y chromosome
2827	15378		2.03	9.8E-01	AF174644.1	NT	Xanopus laevis rec GTPase mRNA, complete cds
3869	16467	28930	0.95	9.8E-01	O67551	SWISSPROT	PROBABLE ENDONUCLEASE IV (ENDODEOXYRIBONUCLEASE IV)
3872	16470	28933	0.61	9.8E-01	BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
3872	16470	28934	0.61	9.8E-01	BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
7250	19779	32634	4.86	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7250	19779	32635	4.86	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7641	20153	33038	1.13	9.8E-01	BF034016.1	EST_HUMAN	601458337F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3860049 5'
7641	20153	33039	1.13	9.8E-01	BF034016.1	EST_HUMAN	601458337F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3860049 5'
8653	21192	34110	0.77	9.8E-01	P38652	SWISSPROT	PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM)
10334	22828		0.56	9.8E-01	AA825565.1	EST_HUMAN	cd55d04.s1 NCI CGAP GC81 Homo sapiens cDNA clone IMAGE:1371847 3'
10874	23395	36410	4.86	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
10874	23395	36411	4.86	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
11597	24040	37109	1.78	9.8E-01	AI680876.1	EST_HUMAN	bt42c10.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2272242 3'
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
12058	24341		1.39	9.8E-01	U52111.2	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9,10,11,12 and optional segments b, c, d and e, partial cds
7212	19743	32597	2.51	9.7E-01	U26716.1	NT	Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds
8440	20980	33895	1.7	9.7E-01	AF149112.1	NT	Trilicium aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds
8446	20986	33901	1.28	9.7E-01	M90544.1	NT	Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (res)

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11049	23562		5.23	9.7E-01	BF511209.1	EST_HUMAN	UI-H-B14-act-e-07-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085140 3'
12858	24728		2.92	9.7E-01	AL114281.1	NT	Bolyris cinerea strain T4 cDNA library under conditions of nitrogen deprivation
4531	17115	29559	0.58	9.6E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4531	17115	29560	0.58	9.6E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4557	17140	29588	1.71	9.6E-01	AW789874.1	EST_HUMAN	PM2-UM0053-240300-005-112 UM0053 Homo sapiens cDNA
5928	18550	31278	3.9	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
5928	18550	31277	3.9	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
8331	20872		1.23	9.6E-01	X95275.1	NT	P. falciparum complete gene map of plastid-like DNA (IR-A)
8785	21324	34248	0.47	9.6E-01	LB1138.1	NT	Rattus norvegicus (strain R21) Rps2r gene, complete cds
9020	21557	34485	0.82	9.6E-01	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
10966	23461	36507	1.81	9.6E-01	AF041427.1	NT	Homo sapiens ribosomal protein s4 Y isoform gene, complete cds
11395	23847	36912	5.18	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'
11395	23847	36913	5.18	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'
11733	24138		2.36	9.6E-01	11421722	NT	Homo sapiens centrosomal protein 2 (CEP2), mRNA
12388	24983	30809	2.8	9.6E-01	U91423.1	NT	Sphyrna tiburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
2515	15079	27851	1.02	9.5E-01	7705591	NT	Homo sapiens CGI-125 protein (LOC51003), mRNA
2681	15248	27817	1.2	9.5E-01	002834	SWISSPROT	ENDOGLUCANASE I PRECURSOR (EGI) (ENDO-1,4-BETA-GLUCANASE)(CELLULOSE I)
3850	16448	28908	1.89	9.5E-01	BE902340.1	EST_HUMAN	601678639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3850	16448	28910	1.89	9.5E-01	BE902340.1	EST_HUMAN	601678639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
8931	21469	34387	0.63	9.5E-01	AI190162.1	EST_HUMAN	qd57607.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1733581 3'
9034	21571	34500	1.07	9.5E-01	AW861102.1	EST_HUMAN	RC1-CT0285-241199-011-b02 C10285 Homo sapiens cDNA
11123	23831	36674	1.71	9.5E-01	BF218771.1	EST_HUMAN	601885163F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103630 5'
11326	23024	36033	1.59	9.5E-01	AW283789.1	EST_HUMAN	UI-H-B12-ahp-f-03-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727677 3'
3235	15847		1.8	9.4E-01	AF165990.1	NT	Bartonella clarridgeiae RNA polymerase beta subunit (rpoB) gene, partial cds
3254	15866		2.47	9.4E-01	AF080595.1	NT	Pimpinella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
8796	21338	34285	0.88	9.4E-01	M80724.1	NT	Human Fc-gamma-receptorIIA (FCGR2A) gene, exon 4
1768	14358		0.95	9.3E-01	AF242382.1	NT	Homo sapiens phytoxy-CoA hydroxylase (PHYH) gene, exon 5
2692	15220	27792	1.09	9.3E-01	BE071172.1	EST_HUMAN	RC5-BT0503-271199-011-B01 BT0503 Homo sapiens cDNA
4107	16701	29154	0.92	9.3E-01	M20218.1	NT	Bovine papillomavirus type 2, complete genome
4107	16701	29155	0.92	9.3E-01	M20218.1	NT	Bovine papillomavirus type 2, complete genome

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5778	18403	31119	1.41	9.3E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5858	18481	31204	3.69	9.3E-01	L36189.1	NT	Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds
8011	20553	33456	1.62	9.3E-01	AA847040.1	EST_HUMAN	ce09b03.s1 NCI_CGAP_OV2 Homo sapiens cDNA clone IMAGE:1385357
8748	21287		1.13	9.3E-01	AF061981.1	NT	Xenopus laevis CCOH zinc finger protein C3H-2 (C3H-2) mRNA, complete cds
8887	21406	34330	1.01	9.3E-01	AL161534.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 34
12508	24829	30893	1.87	9.3E-01	11440288	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 2 (ITPR2), mRNA
12515	24634		2	9.3E-01	AF217207.1	NT	Aedes triseriatus putative large subunit ribosomal protein rpl34 mRNA, complete cds
3276	15937	28369	3.99	9.2E-01	BE622702.1	EST_HUMAN	601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916184 3'
5004	17577		0.62	9.2E-01	BF128973.1	EST_HUMAN	601817814F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4041363 5'
5894	18516		1.41	9.2E-01	7108410	NT	Mus musculus solute carrier family 30 (zinc transporter), member 4 (Slc30e4), mRNA
6140	18754	31512	4.4	9.2E-01	BF037586.1	EST_HUMAN	601461153F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3884681 5'
9578	22078	35042	1.31	9.2E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
9863	22182	35135	1.15	9.2E-01	6871677	NT	Mus musculus carbonic anhydrase 4 (Car4), mRNA
10188	22661	35656	3.47	9.2E-01	11430963	NT	Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA
10314	22808	35800	1.58	9.2E-01	BF593251.1	EST_HUMAN	7c58e06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3578219 3' similar to SW:NU5M_TRYBB
10528	23093	36074	1.75	9.2E-01	BE563811.1	EST_HUMAN	P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5;
11589	24018	37085	2.27	9.2E-01	BF132402.1	EST_HUMAN	601334943F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3888714 5'
1686	14259	26793	4.89	9.1E-01	T96675.1	EST_HUMAN	601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018 5'
2169	14748		2.38	9.1E-01	8923056	NT	ye5270.1.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121369 3' similar to contains Alu repetitive element;
3239	15851	28331	0.93	9.1E-01	T26418.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
3239	15851	28332	0.93	9.1E-01	T26418.1	EST_HUMAN	AB200G8R infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
6315	18922	31699	1.42	9.1E-01	L36033.1	NT	AB200G8R infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8 5'
6830	19226	32031	2.82	9.1E-01	GB1704	SWISSPROT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
7577	20083	32870	15.95	9.1E-01	AA806623.1	EST_HUMAN	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
7719	20227	33115	3.12	9.1E-01	U72995.1	NT	cb71g08.s1 NCI_CGAP_G0B1 Homo sapiens cDNA clone IMAGE:1336862 3'
12093	24976		33.14	9.1E-01	AF050113.1	NT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds
3241	15853	28335	0.81	9.0E-01	7861825	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
3401	16010		0.84	9.0E-01	AL161515.2	NT	Homo sapiens DKFZP564M2423 protein (DKFZP564M2423), mRNA
4488	17054	29498	1.44	9.0E-01	AF099810.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
							Homo sapiens neurexin III-alpha gene, partial cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7424	19948	32814	0.78	9.0E-01	L42547.1	NT	Danio rerio LIM class homeodomain protein (lim5) mRNA, complete cds
7450	19974		1.84	9.0E-01	D38821.1	NT	Xenopus laevis gene for aldolase, complete cds
9271	21797	34748	0.54	9.0E-01	AF088761.1	NT	Danio rerio semaphorin 21a mRNA, complete cds
9744	22242	35223	0.47	9.0E-01	U39702.1	NT	Mycoplasma genitalium section 24 of 51 of the complete genome
							Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete (L1); putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>
5875	18497	31222	2.49	8.9E-01	AF026198.1	NT	Rabbit MHC fragment RLA-DF DNA
6396	18999		1.27	8.9E-01	X60986.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8152	20693		0.47	8.9E-01	AF260225.1	NT	Orithone nana cytochrome-c oxidase subunit 1 (cox) gene, partial cds; mitochondrial gene for mitochondrial product
8365	20605	33824	1.04	8.9E-01	AF259687.1	NT	Xylella fastidiosa, section 90 of 229 of the complete genome
11616	24058	37122	2.59	8.9E-01	AE003944.1	NT	Chlamydia pneumoniae AR39, section 21 of 94 of the complete genome
11927	24282		5.33	8.9E-01	AE002186.2	NT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
4640	17222	29876	2.1	8.8E-01	O26350	SWISSPROT	Pseudorabies virus E6 glycoprotein M gene, complete cds
5576	18207	30658	0.7	8.8E-01	AF310617.1	NT	M. aeruginosa (HUB 5-2-4) DNA from plasmid PNA1
10960	23475	36500	3.82	8.8E-01	Z28337.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719643
11749	25087		2.27	8.8E-01	D90911.1	NT	Homo sapiens SOS1 (SOS1) gene, partial cds
490	13123	25609	1.48	8.7E-01	AF106953.2	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
2446	15013	27585	1.13	8.7E-01	5901883	NT	nm05111.s1 NCL CGAP_P74.1 Homo sapiens cDNA clone IMAGE:1076877
2898	15515	27984	5.67	8.7E-01	AA595863.1	EST_HUMAN	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
4945	17423	29875	0.61	8.7E-01	AF158539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
4845	17423	29876	0.61	8.7E-01	AF158539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
							Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put
5151	17721		3.08	8.7E-01	AF121970.1	NT	RC4-NN0057-120500-013-07 NN0057 Homo sapiens cDNA
7983	20525	33431	0.66	8.7E-01	AW897335.1	EST_HUMAN	qh36606.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846788 3'
8860	21399	34322	0.75	8.7E-01	AI239456.1	EST_HUMAN	qh36606.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846788 3'
8860	21399	34323	0.75	8.7E-01	AI239456.1	EST_HUMAN	qh36606.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1846788 3'
9653	22182	35122	1.7	8.7E-01	AE004963.1	NT	Pseudomonas aeruginosa PAO1, section 524 of 529 of the complete genome
10205	22700	35693	0.56	8.7E-01	BF570169.1	EST_HUMAN	602185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309806 3'
10205	22700	35694	0.56	8.7E-01	BF570169.1	EST_HUMAN	602185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309806 3'
10711	23238	36254	5.79	8.7E-01	BF303970.1	EST_HUMAN	QV0-NN1021-100800-337-03 NN1021 Homo sapiens cDNA
11582	24028	37097	4.31	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
11582	24028	37098	4.31	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12146	24861		4.44	8.7E-01	AV661898.1	EST_HUMAN	AV661898 GLC Homo sapiens cDNA clone GLOGYG07 3'
500	13132		1.55	8.6E-01	X17012.1	NT	Rat IGFI gene for insulin-like growth factor II
891	13505	26024	8.72	8.6E-01	W69089.1	EST_HUMAN	z444e03.r1 Soares_fetal_NbHH19W Homo sapiens cDNA clone IMAGE:343516 5'
2310	14882	27457	1.06	8.6E-01	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
3681	16282	28750	0.78	8.6E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
3870	16468	28931	1.38	8.6E-01	U49724.1	NT	Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds
6057	18674	31415	9.06	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6057	18674	31416	9.06	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6810	19401	32216	1.88	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
6810	19401	32217	1.88	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
7868	20410		1.33	8.6E-01	AP001518.1	NT	Bacillus halodurans genomic DNA, section 12/14
7986	20528	33434	0.54	8.6E-01	AF077837.1	NT	Drosophila melanogaster collapsin response mediator protein (CRMP) mRNA, complete cds
9603	22103		0.48	8.6E-01	AE000979.1	NT	Archaeoglobus fulgidus section 128 of 172 of the complete genome
12338	24812		1.73	8.6E-01	AL112162.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
6826	19416	32232	1.32	8.5E-01	AF165214.1	NT	Bacteriophage D3, complete genome
7533	20053	32926	2.38	8.5E-01	BE542612.1	EST_HUMAN	601067107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453505 5'
7932	20474	33383	0.51	8.5E-01	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
8357	20897	33817	0.84	8.5E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8357	20897	33818	0.84	8.5E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8441	20981	33896	0.51	8.5E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10252	22747	35734	1.38	8.5E-01	AB008799.1	NT	Cyanidium caldarium gene for SigC, complete cds
10252	22747	35735	1.38	8.5E-01	AB008799.1	NT	Cyanidium caldarium gene for SigC, complete cds
12077	24978		3.12	8.5E-01	11418543	NT	Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HIVEP1), mRNA
12084	24355		7.92	8.5E-01	9507008	NT	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), mRNA
4882	17440	29890	0.62	8.4E-01	AF083975.2	NT	Fowl adenovirus 8, complete genome
5685	24747	30807	3.15	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5685	24747	30808	3.15	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
9668	22365		2.68	8.4E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 5/6
771	13390	25889	2.48	8.3E-01	M89437.1	NT	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3129	15743	28212	3.26	8.3E-01	AL161506.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3883	16481	28943	0.66	8.3E-01	AB010879.1	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
4084	16680	29140	3.24	8.3E-01	Y19177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
5473	18107	30426	2.15	8.3E-01	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9587	22087		3.14	8.3E-01	AI791962.1	EST_HUMAN	nn01f12.y5 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR.11 THR repetitive element;
10019	22514	35507	1.11	8.3E-01	AF098070.1	NT	Drosophila melanogaster Lis1 homolog mRNA, complete cds
10119	22814	35804	3.5	8.3E-01	AF108133.1	NT	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds
10553	23089	36103	2.92	8.3E-01	AE000903.1	NT	Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 109 of 148) of the complete genome
10571	23108		2.92	8.3E-01	7212472	NT	Phytophthora infestans mitochondrion, complete genome
11183	23888	36735	2.45	8.3E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
2098	14875	27244	3.23	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2137	14715		1.45	8.2E-01	AF145589.1	NT	Mus musculus trophinin (Tnn) gene, complete cds
3969	16567	28036	1.12	8.2E-01	AB014574.1	NT	Homo sapiens mRNA for KIAA0674 protein, partial cds
4209	16788	29246	0.61	8.2E-01	Z72584.1	NT	S.cerevisiae chromosome VII reading frame ORF YGL082w
4209	16788	29247	0.61	8.2E-01	Z72584.1	NT	S.cerevisiae chromosome VII reading frame ORF YGL082w
5270	17832	30258	1.08	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
5420	17977	30385	2.11	8.2E-01	AB028957.1	NT	Homo sapiens mRNA for KIAA1034 protein, partial cds
6871	19605	32439	0.8	8.2E-01	AJ010142.1	NT	Amanita muscaria mRNA for SC1125 protein
6978	19554	32378	3.18	8.2E-01	AW379433.1	EST_HUMAN	CM4-HT0243-081199-037-e01 HT0243 Homo sapiens cDNA
7313	24779	32700	4.21	8.2E-01	Z12126.1	NT	S.cerevisiae MET, LEU4, and POL1 genes encoding MET4 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)
9938	22433	35409	0.63	8.2E-01	AB014530.1	NT	Homo sapiens mRNA for KIAA0630 protein, partial cds
9971	22466	35450	1.67	8.2E-01	AF032859.1	NT	Homo sapiens thiodoxin-related protein mRNA, complete cds
10123	22618	35609	0.59	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10123	22618	35610	0.59	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10266	22781	35772	3.52	8.2E-01	Q8J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
10286	22781	35773	3.52	8.2E-01	Q8J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
11488	23947	37017	3.33	8.2E-01	L10127.1	NT	Mollusca contagiosum virus type 1 ORF1 and ORF2 DNA
11578	24022	37091	8.05	8.2E-01	P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
11583	24028	37099	5.68	8.2E-01	H87398.1	EST_HUMAN	yw14d02.r1 Soares_placenta_8to6weeks_2NHP8b9W Homo sapiens cDNA clone IMAGE:252195 5' similar to gb:M36072.60S RIBOSOMAL PROTEIN L7A (HUMAN);
12102	24364	30970	1.86	8.2E-01	AJ001261.1	NT	Mus musculus mRNA for NIPSNAP2 protein
2787	15340		1.79	8.1E-01	AF191839.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3504	16108	28585	2.89	8.1E-01	AF055066.1	NT	Homo sapiens MHC class I region
3504	16108	28586	2.89	8.1E-01	AF055066.1	NT	Homo sapiens MHC class I region

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5046	17619		0.68	8.1E-01	AF202634.1	NT	Drosophila melanogaster NaK-ATPase beta subunit isoform 4 (JYbeta2) mRNA, complete cds
6457	19058	31843	0.88	8.1E-01	U16790.1	NT	Mus musculus putative collagen alpha-2(XI) chain (COL11A2) gene, partial cds
6735	19329	32134	2.54	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M8-B
6735	19329	32135	2.54	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M8-B
							Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nac) and putative amylose-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cd>
7652	20394	33298	0.84	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nac) and putative amylose-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cd>
7652	20394	33299	0.84	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nac) and putative amylose-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cd>
8545	21084	34006	0.92	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
8545	21084	34007	0.92	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
							xx01h03.x1 NCJ CGAP Kid11 Homo sapiens cDNA clone IMAGE:2692469 3' similar to SW.LYAR_MOUSE Q08288 CELL GROWTH REGULATING NUCLEOLAR PROTEIN, contains MER22.b1 PTR5 repetitive element:
8705	21244	34167	1.08	8.1E-01	AW242647.1	EST_HUMAN	PROBABLE E4 PROTEIN
10032	22527	35522	0.54	8.1E-01	P06425	SWISSPROT	RCO-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
11356	23810	36869	2.97	8.1E-01	BE838558.1	EST_HUMAN	RCO-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
11356	23810	36870	2.97	8.1E-01	BE838558.1	EST_HUMAN	RCO-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
11811	24183	31031	3.32	8.1E-01	AE001711.1	NT	Thermotoga maritima section 23 of 136 of the complete genome
188	12849		4.99	8.0E-01	AJ271510.1	NT	Staphylococcus aureus partial pla gene for phosphate acyltransferase allele 15
310	12885	25453	7.95	8.0E-01	AJ132772.1	NT	Bos taurus tub and rtf genes
2080	14661		1.47	8.0E-01	BF830962.1	EST_HUMAN	602072473F1 NCJ CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215091 5'
3113	15728	28189	1.24	8.0E-01	AF127897.1	NT	Saimiri boliviensis olfactory receptor (SBO27) gene, partial cds
3354	15862	28439	1.13	8.0E-01	AB006193.1	NT	Mus musculus gene for oviductal glycoprotein, complete cds
3765	16366		1.05	8.0E-01	AL162758.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 7/7
4830	17213	28664	5.95	8.0E-01	X63739.2	NT	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
5117	17689	30127	1.09	8.0E-01	7657352	NT	Mus musculus myosin IXb (Myo9b), mRNA
7931	20473		2.32	8.0E-01	AW901489.1	EST_HUMAN	RCO-NN1012-270300-021-h06 NN1012 Homo sapiens cDNA
8462	21002	33819	1.17	8.0E-01	Y11095.1	NT	Rice stripe virus RNA 3
479	13112	25602	1.37	7.9E-01	D11476.1	NT	Lymnaea dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
744	13364		1.05	7.9E-01	AE002130.1	NT	Ureaplasma urealyticum section 31 of 59 of the complete genome
1648	14240		28.9	7.9E-01	AB040885.1	NT	Homo sapiens mRNA for KIAA1452 protein, partial cds
1695	14288		1.11	7.9E-01	U32739.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2303	14876	27452	6.78	7.9E-01	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitsugumin29, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2304	14877	27453	5.48	7.9E-01	AF130459.1	NT	Danio rerio Trp4-associated protein Tap1A (lap1A) mRNA, complete cds
3567	16171	28653	2.33	7.9E-01	AF228664.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4389	16975		0.76	7.9E-01	BE263812.1	EST_HUMAN	601192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5'
4717	17268	28743	1.04	7.9E-01	8753745	NT	Mus musculus embigin (Emb), mRNA
4717	17268	28744	1.04	7.9E-01	8753745	NT	Mus musculus embigin (Emb), mRNA
5315	17877		5.8	7.9E-01	M28930.1	NT	Human insulin receptor (allele 2) gene, exons 14, 15, 16 and 17
6485	19066	31868	0.69	7.9E-01	D38145.1	NT	Human mRNA for prostacyclin synthase, complete cds
8053	20595	33502	2.52	7.9E-01	X80906.1	NT	P. salivum GR gene
8466	21981	34948	4.67	7.9E-01	U01812.1	NT	Giardia lamblia variant-specific surface protein G3M-B (vspG3M-B) mRNA, partial cds
9862	22457	35440	4.27	7.9E-01	P19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
10003	22498	35487	0.75	7.9E-01	AV700860.1	EST_HUMAN	AV700860 GK Homo sapiens cDNA clone GKCDRE12 3'
10405	22869	35894	0.71	7.9E-01	AB000631.1	NT	Streptococcus mutans DNA for sigma 42 protein, dTDP-4-keto-L-rhamnose reductase, complete cds
10886	23407		2.28	7.9E-01	7662471	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
11089	23801	36839	2.72	7.9E-01	P19022	SWISSPROT	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
909	13522		1.4	7.8E-01	Z43785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04
2314	14866	27481	1.4	7.8E-01	AW959587.1	EST_HUMAN	EST371637 MAGE sequences, MAGF Homo sapiens cDNA
4811	17388	29840	0.81	7.8E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5189	17754		0.81	7.8E-01	AW753353.1	EST_HUMAN	RC3-CT0254-130100-023-c02 C10254 Homo sapiens cDNA
6219	18828	31603	2.33	7.8E-01	AF115856.1	NT	Sphenodon punctatus alpha endase mRNA, partial cds
6367	18971	31750	1.05	7.8E-01	P05231	SWISSPROT	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR)
6589	19186	31988	0.75	7.8E-01	AL445068.1	NT	Thermoplasma acidophilum complete genome, segment 4/5
8428	20688	33881	1.04	7.8E-01	BF108927.1	EST_HUMAN	7154405.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525178 3'
9160	21695	34639	1.02	7.8E-01	Y10159.1	NT	D discoideum recGAP gene
9255	21761	34733	0.53	7.8E-01	4826873	NT	Homo sapiens nucleoporin 214kD (CAIN) (NUP214), mRNA
10031	22526		0.78	7.8E-01	Q25452	SWISSPROT	MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1)
12071	24957		2.33	7.8E-01	L28260.1	NT	Arabidopsis thaliana 1-amino-1-cyclopropanecarboxylate synthase (ACS6) gene, complete cds
150	12813	25300	4.65	7.7E-01	AF184345.1	NT	Lycopodium obscurum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
755	13374		1.44	7.7E-01	AF050157.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IiEbeta) and major histocompatibility protein class II beta chain (IiEbeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-li>
2737	15292	27860	2.33	7.7E-01	O33915	SWISSPROT	CITRATE SYNTHASE

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3400	16009		0.62	7.7E-01	8393408	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GALNAC-T7) (GALNAC-T7), mRNA
3660	16262	28734	4.78	7.7E-01	AF118085.1	NT	Homo sapiens PRO1975 mRNA, complete cds
4486	17071	29521	3.17	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
4486	17071	29522	3.17	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
5749	18375	31084	1.33	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5749	18375	31085	1.33	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
6110	18726	31479	0.8	7.7E-01	R08600.1	EST_HUMAN	yf24b02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127755 3'
9758	22256	35239	0.82	7.7E-01	AB021134.1	NT	Daphnia magna hemoglobin gene cluster (dhb3, dhb1 and dhb2 genes), complete cds
11957	24280		15.01	7.7E-01	11497621	NT	Archaeoglobus fulgidus, complete genome
4790	17370	29822	19.73	7.6E-01	L27316.1	NT	Oryctolagus cuniculus immunoglobulin VDJ region gene
4790	17370	29823	19.73	7.6E-01	L27316.1	NT	Oryctolagus cuniculus immunoglobulin VDJ region gene
6248	18857	31628	4.81	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
8248	18857	31629	4.81	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6641	19237	32039	0.7	7.6E-01	P37938	SWISSPROT	MATING-TYPE PROTEIN A-ALPHA Z4
6935	18043	30465	0.95	7.6E-01	A1253399.1	EST_HUMAN	aq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
6935	18043	30488	0.95	7.6E-01	A1253399.1	EST_HUMAN	aq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
7113	19453	32269	0.98	7.6E-01	U72487.1	NT	Rattus norvegicus calcium-independent alpha-latrotoxin receptor mRNA, complete cds
8009	20551	33455	1.34	7.6E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; PthLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (Pft27) gene, complete cds; and H5AR (H5ar) gene, complete cds
8068	20610	33522	1.76	7.6E-01	8857752	NT	Mus musculus advillin (Advil-pending), mRNA
8068	20610	33523	1.76	7.6E-01	8857752	NT	Mus musculus advillin (Advil-pending), mRNA
8267	20808	33727	0.55	7.6E-01	Q01098	SWISSPROT	GLUTAMATE (NMMA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
8267	20808	33728	0.55	7.6E-01	Q01098	SWISSPROT	GLUTAMATE (NMMA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
8997	21435	34359	0.91	7.6E-01	6753577	NT	Mus musculus cytochrome P450, 2b9, phenobarbital inducible, type a (Cyp2b9), mRNA
9203	21720	34684	3.33	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
9203	21720	34685	3.33	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
11236	23767	36824	2.74	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
11236	23767	36825	2.74	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11556	24004		5.74	7.6E-01	AL161592.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
11711	24121		6.31	7.6E-01	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
539	13170		1.32	7.5E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
610	13238	25712	1.13	7.5E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
7530	20050	32923	0.74	7.5E-01	AF052730.1	NT	Drosophila melanogaster tyrosine kinase receptor protein (eph) mRNA, complete cds
12027	24318		5.28	7.5E-01	AF163151.2	NT	Homo sapiens dentin sialophosphoprotein precursor (DSPP) gene, complete cds
12522	24638	30897	1.91	7.5E-01	D80907.1	NT	Synechocystis sp. PCC6803 complete genome, 9/27, 1058467-1188885
1169	13771	28279	1.38	7.4E-01	AI598146.1	EST_HUMAN	tn14b09.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element; contains element MIR repetitive element;
3789	16389	28854	0.93	7.4E-01	AF112538.1	NT	Malva pusilla actin (Act1) mRNA, complete cds
4400	16985	29430	7.7	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
7785	20328	33234	1.03	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
7785	20328	33235	1.03	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8588	21107	34028	0.93	7.4E-01	BF346266.1	EST_HUMAN	602018456F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4154340 5'
8847	21188		0.64	7.4E-01	U87980.1	NT	Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon
9028	21563	34492	7.17	7.4E-01	BE747503.1	EST_HUMAN	601573026F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'
9083	21819	34554	1.19	7.4E-01	AA187986.1	EST_HUMAN	zp87h01.s1 Strategene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:625267 3' similar to SW:TCPOQ_MOUSE_P42932 T-COMPLEX PROTEIN 1, THETA SUBUNIT;
10301	22795	35788	0.59	7.4E-01	11424933	NT	Homo sapiens NY-REN-45 antigen (LOC51133), mRNA
11516	23984	37034	1.88	7.4E-01	AB021480.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
11516	23984	37035	1.88	7.4E-01	AB021480.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
11677	24086		4.11	7.4E-01	6753217	NT	Mus musculus complement component 1 inhibitor (C1inh), mRNA
11784	24175		1.28	7.4E-01	AA72641.1	EST_HUMAN	ta13h01.x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2043985 3'
4723	17304	28748	0.72	7.3E-01	AE001186.1	NT	Borrelia burgdorferi (section 52 of 70) of the complete genome
4810	17388	29839	2.93	7.3E-01	AF225421.1	NT	Homo sapiens HT017 mRNA, complete cds
5280	17823	30248	0.99	7.3E-01	O43103	SWISSPROT	FERRICHRONE SIDEROPHORE PEPTIDE SYNTHETASE
6720	19314	32116	5.86	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
6720	19314	32117	5.86	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
7151	24777	32525	0.82	7.3E-01	AJ011418.1	NT	Lycopodium esculentum mRNA for ubiquitin activating enzyme
7549	20088	32942	7.77	7.3E-01	M28511.1	NT	V.alginolyticus sucrose (scrB) gene, complete cds
7549	20088	32943	7.77	7.3E-01	M28511.1	NT	V.alginolyticus sucrose (scrB) gene, complete cds
11307	23800	36859	3.86	7.3E-01	AA4876019.1	EST_HUMAN	225808.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431789 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11307	23800	36860	3.86	7.3E-01	AA678019.1	EST_HUMAN	z25b08.s1 Soares fetal liver spleen 1NfLS S1 Homo sapiens cDNA clone IMAGE:431799 3'
864	13479		1.68	7.2E-01	L29281.1	NT	Rattus norvegicus initiation factor-2 kinase (eIF-2a) mRNA, complete cds
2000	14582	27141	3.04	7.2E-01	X79140.1	NT	N'tabacum NalF-4A13 mRNA
2501	15065	27639	1.36	7.2E-01	AB009605.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3103	15718	28188	1.29	7.2E-01	AF198100.1	NT	Fowlpox virus, complete genome
3500	16105	28580	2.97	7.2E-01	AF065606.1	NT	Giardia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-6/A-I allele, complete cds
3640	16538	29005	1.81	7.2E-01	BF338350.1	EST_HUMAN	602035589F1 NCL CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183222 5'
4185	16775	29222	0.6	7.2E-01	U02598.1	NT	Dictyocaulus viviparus nematode polyprotein antigen precursor (DVA) mRNA, complete cds
4884	17459	29811	2.54	7.2E-01	D90314.1	NT	L. mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
5348	17908	30323	0.9	7.2E-01	AF158600.2	NT	Streptococcus thermophilus bacteriophage Sf111, complete genome
5386	17945	30358	0.59	7.2E-01	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
7265	19793	32649	0.82	7.2E-01	U69833.1	NT	Solanum tuberosum cold-stress inducible protein (C17) gene, complete cds
8391	20931	33851	1.15	7.2E-01	AF236061.1	NT	Oryzobolus cuniculus RING-finger binding protein mRNA, partial cds
8893	21431		0.53	7.2E-01	AV743773.1	EST_HUMAN	AV743773 CB Homo sapiens cDNA clone CBMAFD06 5'
10243	22738	35729	2.14	7.2E-01	BF670061.1	EST_HUMAN	602118381F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4275381 5'
10618	23150	36162	5.23	7.2E-01	U82823.1	NT	Rattus norvegicus cytochrome mRNA, complete cds
12037	16775	29222	1.66	7.2E-01	U02568.1	NT	Dictyocaulus viviparus nematode polyprotein antigen precursor (DVA) mRNA, complete cds
12233	24449		4.42	7.2E-01	AP000063.1	NT	Aeropyrum pernix genomic DNA, section 67
12266	24995		1.67	7.2E-01	Y10188.1	NT	B. thuringiensis PK1 & cap genes, putative
721	13341	25831	10.56	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform (RyR1), complete cds
3098	15713	28185	18.71	7.1E-01	AJ270777.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16
4287	16873	29321	4.11	7.1E-01	7305360	NT	Mus sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16
4287	16873	29322	4.11	7.1E-01	7305360	NT	Mus musculus otogelin (Otog), mRNA
6103	18719	31471	1.81	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4286344 5'
6103	18719	31472	1.81	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4286344 5'
7029	19563	32390	6.04	7.1E-01	U36232.1	NT	Drosophila melanogaster 6-pyruvoylterahydropterin synthase (pr) gene, complete cds
8132	20673	33564	0.53	7.1E-01	H54244.1	EST_HUMAN	y488409.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:202861 3'
8671	21210	34128	0.78	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301299-011-d09 BT0567 Homo sapiens cDNA
8671	21210	34129	0.78	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301299-011-d09 BT0567 Homo sapiens cDNA
9769	22267	35252	1.48	7.1E-01	BE044405.1	EST_HUMAN	601496330F1 NIH_MGC 70 Homo sapiens cDNA clone IMAGE:3898495 5'
10309	22803	35795	1.06	7.1E-01	M12861.1	NT	Human T-cell receptor gamma-chain J2 gene
12012	24978		2.58	7.1E-01	AA421492.1	EST_HUMAN	zu06h11.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:731109 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1272	13868	26387	1.3	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
1272	13868	26388	1.3	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
2492	15057	27630	1.22	7.0E-01	N62412.1	EST_HUMAN	yz73e07 s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element
2492	15057	27631	1.22	7.0E-01	N62412.1	EST_HUMAN	yz73e07 s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element
5213	17778		1.98	7.0E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
5382	17922	30338	2.99	7.0E-01	AE003921.1	NT	Xyella fastidiosa, section 67 of 228 of the complete genome
6107	18723		1.03	7.0E-01	AB021316.1	NT	Arabidopsis thaliana mRNA for chlorophyll b synthase, complete cds
8319	20860		11.92	7.0E-01	AE000253.1	NT	Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome
9240	21766	34714	0.61	7.0E-01	U53868.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mtlA, mtlR, mtlF, and mtlD genes, complete cds
9240	21766	34715	0.61	7.0E-01	U53868.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mtlA, mtlR, mtlF, and mtlD genes, complete cds
10959	23513	36546	1.99	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
10959	23513	36547	1.99	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
12594	24918	30715	1.35	7.0E-01	9630464	NT	Bacteriophage N15 virion, complete genome
1005	13616	26130	10.2	6.9E-01	U68674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1005	13616	26131	10.2	6.9E-01	U68674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1353	13948	26472	2.8	6.9E-01	AA503530.1	EST_HUMAN	nn28a09.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085176 3'
3256	15868	26348	1.7	6.9E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
5954	18576	31310	0.8	6.9E-01	AB039692.1	NT	Branchiostoma belcheri BbNA3 mRNA for ribonuclease, complete cds
6508	19108	31803	1.31	6.9E-01	BE296188.1	EST_HUMAN	601177333F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532328 5'
7921	20463	33369	3.4	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
7921	20463	33370	3.4	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
9098	21634		0.83	6.9E-01	AF118046.1	NT	Entamoeba dispar cation transporting ATPase (atpase) gene, partial cds
9611	22111	35073	0.62	6.9E-01	AF206319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
9611	22111	35074	0.62	6.9E-01	AF206319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
10307	22801	35793	0.66	6.9E-01	BF242367.1	EST_HUMAN	601880580F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109419 5'
11138	23646	36687	1.94	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
11138	23646	36688	1.94	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11651	24870		2.36	6.9E-01	Q99958	SWISSPROT	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK HEAD PROTEIN 1) (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL14)
12870	25003	30611	1.33	6.9E-01	A1888312.1	EST_HUMAN	wn3102.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2447087 3'
992	13804	26118	1.28	6.8E-01	AF017784.1	NT	Giardia intestinalis carbamyl kinase gene, complete cds
2898	16265		1.25	6.8E-01	D90917.1	NT	Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470
2856	14249	26783	1.62	6.8E-01	AA854475.1	EST_HUMAN	q175a05.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1402256 3' similar to gb:X58411_ma1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
4872	17254	29708	1.45	6.8E-01	J00762.1	NT	Rat(hooded) prolactin gene : exon iii and flanks
9556	22056	35017	2.11	6.8E-01	AB037766.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
10261	22756		0.48	6.8E-01	AA687936.1	EST_HUMAN	nv13e07.s1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:1220100 3' similar to gb:X13546_ma1 Human HMG-17 gene for non-histone chromosomal protein (HUMAN);
10965	23480	36506	2.96	6.8E-01	AJ276875.1	NT	Stagonospora avenae bgl1 gene for beta-glucosidase, exons 1-4
10965	23480	36506	2.96	6.8E-01	AJ276875.1	NT	Stagonospora avenae bgl1 gene for beta-glucosidase, exons 1-4
10983	23507	36540	2.16	6.8E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
10983	23507	36541	2.16	6.8E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11178	23684	36730	2.2	6.8E-01	AF164151.1	NT	Anopheles gambiae strain M2 translation initiation factor 4C(1A) (eIF-4C) mRNA, complete cds
11475	23925	36995	1.77	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RaIGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
11475	23925	36996	1.77	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RaIGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
320	12974	25463	27.63	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
361	13010	25493	26.51	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
1955	14539		0.97	6.7E-01	M12132.1	NT	Quail fast skeletal muscle troponin I gene, complete cds
2192	14768	27340	1.65	6.7E-01	AA451864.1	EST_HUMAN	zx12g12.s1 Soares_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:766310 3' similar to contains element TAR1 repetitive element ;
2211	15460	27361	2.66	6.7E-01	AF186073.1	NT	Drosophila melanogaster Mst85C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
3026	15642	28120	4.28	6.7E-01	6675580	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4550	17133	29581	0.64	6.7E-01	X74421.1	NT	S. tuberosum mRNA for glucose-6-phosphate dehydrogenase

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5100	17672	30111	0.96	6.7E-01	AW079110.1	EST_HUMAN	xa95g12.x1 NCI_CGAP_Col17 Homo sapiens cDNA clone IMAGE:2574598 3'
5700	18326	30829	0.8	6.7E-01	J04836.1	NT	M.barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
5700	18326	30830	0.8	6.7E-01	J04836.1	NT	M.barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
6116	18732	31485	0.83	6.7E-01	AE001486.1	NT	Haicobacter pylori, strain J99 section 47 of 132 of the complete genome
6465	19066	31851	1.55	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
6465	19066	31852	1.55	6.7E-01	9635035	NT	Gallid herpesvirus 2, complete genome
7358	19892		4.12	6.7E-01	AE004608.1	NT	Pseudomonas aeruginosa PA01, section 167 of 529 of the complete genome
7378	19904	32768	0.9	6.7E-01	AE001486.1	NT	Haicobacter pylori, strain J99 section 47 of 132 of the complete genome
10049	22544		0.87	6.7E-01	M34046.1	NT	Human placental protein 14 (PP14) gene, complete cds
10832	23353	36368	2.52	6.7E-01	BF354649.1	EST_HUMAN	CM8-H10769-010600-197-c03 H10769 Homo sapiens cDNA
11333	23031	36040	3.45	6.7E-01	O14357	SWISSPROT	N-ACETYLGLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GP11
2546	15110	27682	2.66	6.6E-01	AF075240.1	NT	Homo sapiens SLIT1 protein (SLIT1) mRNA, partial cds
2724	15279	27846	1.01	6.6E-01	AF198339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3536	16141	28623	1.35	6.6E-01	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMAGA) mRNA
3719	16320	28788	3.42	6.6E-01	Y07869.1	NT	C.albicans random DNA marker, 282bp
4187	16777		0.67	6.6E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5227	17791	30210	0.97	6.6E-01	AI218230.1	EST_HUMAN	q23a10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845498 3' similar to contains PTR5.b2 MER28 repetitive element;
6474	18075	31858	4.22	6.6E-01	6880577	NT	Mus musculus kinesin light chain 2 (Klc2), mRNA
7675	20186	33074	3.61	6.6E-01	AV660506.1	EST_HUMAN	AV660506 GLC Homo sapiens cDNA clone GLGID04.3'
8501	21040	33961	0.84	6.6E-01	AV704700.1	EST_HUMAN	AV704700 ADB Homo sapiens cDNA clone ADBCAF11 5'
9582	22082		1.73	6.6E-01	AL183278.2	NT	Homo sapiens chromosome 21 segment HS21C078
9915	22411		0.66	6.6E-01	AU118198.1	EST_HUMAN	AU118198 HEMBA1 Homo sapiens cDNA clone HEMBA1003079 5'
12118	24377	30973	1.27	6.6E-01	AF10001.1	NT	Homo sapiens guanylate cyclase activating protein 3 (GCAP3) gene, exon 4 and complete cds
651	13274	25751	1.12	6.5E-01	M75140.1	NT	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
651	13274	25752	1.12	6.5E-01	M75140.1	NT	H.vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3480	16086	28560	5.04	6.5E-01	AB041225.1	NT	Mus musculus gene for Tob2, complete cds
4110	16704	29157	1.1	6.5E-01	4504632	NT	Homo sapiens interleukin 10 receptor, alpha (IL10RA) mRNA
4369	16956	29398	3.29	6.5E-01	AJ272285.1	NT	Homo sapiens SP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
4699	17281	29726	1.28	6.5E-01	D00594.1	NT	Oryza sativa gene for prepro-glutelin, exons 1, 2, 3, 4, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5219	17784	30202	2.39	6.5E-01	U28921.1	NT	Phaseolus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
5336	17897	30312	1.02	6.5E-01	Z70628.1	NT	H sapiens mRNA for immunoglobulin heavy chain variable region (9D4-A6, VH4, 4-59/DP-71)
6825	19415	32231	1.26	6.5E-01	D88348.1	NT	Chicken mRNA for 115-kDa melanosomal matrix protein, complete cds
7663	20175	33082	0.96	6.5E-01	A798982.1	EST_HUMAN	wc46a02.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2321642 3'
9751	22249		1.25	6.5E-01	T78904.1	EST_HUMAN	yd21b04.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:108847 3'
10238	22733	35725	2.49	6.5E-01	AF119876.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
10512	23050	36061	3.35	6.5E-01	H87583.1	EST_HUMAN	yu17706.r1 Soares placenta_8tc9weeks_2NbhP8lc9W Homo sapiens cDNA clone IMAGE:252515 5'
10568	23102	36116	4.35	6.5E-01	AA601287.1	EST_HUMAN	no15c07.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100748 3'
10669	23201		4.29	6.5E-01	AU138078.1	EST_HUMAN	AU138078 PLACE1 Homo sapiens cDNA clone PLACE1007810 5'
11470	23920	36989	2.7	6.5E-01	AF014115.1	NT	Plasmodium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
12067	24348		8.24	6.5E-01	BE465050.1	EST_HUMAN	ht74a10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130 3'
12321	24817		3.04	6.5E-01	Z74145.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL097c
273	12930	25417	9.34	6.4E-01	U48948.1	NT	Drosophila melanogaster 8kd dynein light chain mRNA, complete cds
3502	16107	28583	3.78	6.4E-01	U48854.2	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cds
3928	16526	28993	1.33	6.4E-01	AB046827.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
4591	17174	29619	0.66	6.4E-01	Y12488.1	NT	M.musculus whn gene
4591	17174	29620	0.66	6.4E-01	Y12488.1	NT	M.musculus whn gene
5402	17860	30371	0.97	6.4E-01	AE002551.2	NT	Neisseria meningitidis serogroup B strain MC58 section 193 of 206 of the complete genome
8549	21088	34010	1.78	6.4E-01	AE001247.1	NT	Treponema pallidum section 63 of 87 of the complete genome
10001	22496	35486	8.26	6.4E-01	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
10015	22510	35501	1.16	6.4E-01	BF070405.1	EST_HUMAN	602150289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291126 5'
12188	24420		29.97	6.4E-01	AV759212.1	EST_HUMAN	AV759212 MDS Homo sapiens cDNA clone MDSGCC09 5'
459	13093	25587	3.75	6.3E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PHRP-III)
560	13191	25689	56.3	6.3E-01	U32689.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2207	14783	27356	3.24	6.3E-01	U81136.1	NT	Shigella flexneri multi-antibiotic resistance locus
2614	15176	27744	2.78	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2614	15176	27745	2.78	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
3050	15666		0.75	6.3E-01	Y11275.1	NT	Lycopodium obscurum p69a gene, complete CDS
6214	18924	31595	0.78	6.3E-01	BE093906.1	EST_HUMAN	PMO-B10757-010500-002-a05 B10757 Homo sapiens cDNA
6712	18306	32110	1	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds
6712	19306	32111	1	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8458	20988		3.32	6.3E-01	BE902044.1	EST_HUMAN	601876889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958351 5'
8819	21358	34284	0.91	6.3E-01	SG2927.1	NT	glycoprotein IIIa [Alu 1 and 3 fusion junction] [human, Genomic Mutant, 300 nt]
9147	21682	34627	1.15	6.3E-01	BF216984.1	EST_HUMAN	601884050F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4102586 5'
9341	21855	34804	2.9	6.3E-01	9627521	NT	Varicella virus, complete genome
9341	21855	34805	2.9	6.3E-01	9627521	NT	Varicella virus, complete genome
9851	22349		0.67	6.3E-01	AE002329.2	NT	Chlamydia muridarum, section 59 of 85 of the complete genome
10324	22818	35814	1.52	6.3E-01	Z73003.1	NT	S. cerevisiae chromosome VII reading frame ORF YGR218w
10421	22915	35915	0.87	6.3E-01	AE000313.1	NT	Escherichia coli K-12 MG1685 section 203 of 400 of the complete genome
							nr09h06.s1 NCJ_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:002916 O02816
10839	23456	36479	2.45	6.3E-01	AA877715.1	EST_HUMAN	HLARK.
11216	23719	36773	15.21	6.3E-01	AB04160.1	EST_HUMAN	CM-BT043-090298-046 BT043 Homo sapiens cDNA
11302	23795	36853	1.94	6.3E-01	P47003	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION
11458	23908	36975	2.02	6.3E-01	P36073	SWISSPROT	HYPOTHETICAL 15.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION
11769	25042	30505	30.63	6.3E-01	9810293	NT	Mus musculus keratin complex 2, gene 6g (K12-6g), mRNA
11864	24219		1.85	6.3E-01	AF106227.1	NT	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPSS) mRNA, complete cds
12082	24063		3.2	6.3E-01	X83528.1	NT	Climicola pecD gene
5175	17742	30171	0.71	6.2E-01	AF157898.1	NT	Spermophilus suslicus isolate S47 cytochrome b (cytb) gene, complete cds; mitochondrial gene for
6030	18649	31390	2.03	6.2E-01	Q10135	SWISSPROT	mitochondrial product
7506	20028		3.14	6.2E-01	AF022253.1	NT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME1
							Mus musculus calcium-sensing receptor related protein 4 (Casr-rs4) mRNA, partial cds
7548	24786	32841	1.08	6.2E-01	AL021127.2	NT	Mus musculus chromosome X contigA; putative Magea8 gene, Caltratin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
8243	20784	33703	5.65	6.2E-01	H72955.1	EST_HUMAN	ys01e08.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:213542 3'
8780	21328	34254	0.54	6.2E-01	AF034411.1	NT	Lycopodium esculentum cytosolic Cu,Zn superoxide dismutase (Sod) gene, partial cds; and dehydroquinase
9370	20309	33212	1.75	6.2E-01	BE562687.1	EST_HUMAN	dehydratase/shikimate:NADP oxidoreductase gene, complete cds
9429	21938		2.35	6.2E-01	M24461.1	NT	601336146F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690010 5'
9990	22485	35472	5.85	6.2E-01	AL161511.2	NT	Human pulmonary surfactant-associated protein SP-B (SFTPB) mRNA, complete cds
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
10429	22823	35927	3.76	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOI
							PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
10429	22823	35928	3.76	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE; THIOI
							PROTEASE P3C; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
2438	15005		4.95	6.1E-01	6678076	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA
4632	17215	29666	1.05	6.1E-01	4657538	NT	Homo sapiens solute carrier family 26 (sulfate transporter), member 2 (SLC26A2) mRNA

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5141	17712	30142	1.09	6.1E-01	L20427.1	NT	Rattus norvegicus dihydroxyphenylbenzoate methyltransferase mRNA, complete cds
5141	17712	30143	1.09	6.1E-01	L20427.1	NT	Rattus norvegicus dihydroxyphenylbenzoate methyltransferase mRNA, complete cds
5727	18353	31057	1.54	6.1E-01	M59940.1	NT	Caenorhabditis elegans N2 Cdklyd (h1h-1) alternatively spliced genes, complete cds
6951	19528	32351	3.55	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
6951	19528	32352	3.55	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
8175	20716	33632	3.57	6.1E-01	AF033535.1	NT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
8730	21269	34187	1.23	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
8730	21269	34188	1.23	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
9336	21850	34798	19.4	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9336	21850	34799	19.4	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9756	22254	35236	1.15	6.1E-01	AE004452.1	NT	Pseudomonas aeruginosa PAO1, section 13 of 529 of the complete genome
9859	22454	35436	1.8	6.1E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
10837	23358		8.53	6.1E-01	X74507.1	NT	P.sativum mdh mRNA for chloroplast malate dehydrogenase (NADP+)
11581	24027	37095	2.19	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
11581	24027	37096	2.19	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
12530	24643		1.91	6.1E-01	X95287.1	NT	M.maza orfA, orfB, and orfC of archaeal ABC-transporter system
520	13152	25635	1.46	6.0E-01	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
587	13217		3.41	6.0E-01	5802999	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA
1406	13999	26528	1.93	6.0E-01	AF065253.1	NT	Human respiratory syncytial virus strain CH93-53b attachment protein (G) gene, complete cds
3887	16485	28946	0.86	6.0E-01	AJ233386.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71
4287	18853		1.16	6.0E-01	AF058895.1	NT	Homo sapiens Notch3 (NOTCH3) gene, exons 26, 27, and 28
5485	18119	30526	1.93	6.0E-01	P20288	SWISSPROT	D(2) DOPAMINE RECEPTOR
5631	18260	30732	2.28	6.0E-01	AW139713.1	EST_HUMAN	U1-H-B11-aab-a-10-Q-U1 st NC1 CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718619 3'
6660	19256	32059	3.73	6.0E-01	U38813.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds
6767	19360	32169	0.79	6.0E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON)
7391	19918	32780	5.29	6.0E-01	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8066	20608	33520	4.72	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
8066	20608	33521	4.72	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
9737	22235	35214	2.22	6.0E-01	AB008193.1	NT	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10174	22669		1.61	6.0E-01	Q01497	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PER8 (PEROXIN-3)
10836	23453	36476	2.14	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
10836	23453	36477	2.14	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
11426	23877	36942	2.84	6.0E-01	AI420823.1	EST_HUMAN	U08107.x1 NCI_OGAP_P728 Homo sapiens cDNA clone IMAGE:2095621 3'
12158	24398	30978	1.82	6.0E-01	11421663	NT	Homo sapiens nuclear factor (erythroid-derived 2) like 3 (NFE2L3), mRNA
12265	24475		1.99	6.0E-01	AA706087.1	EST_HUMAN	zj96g05.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462776 3'
12426	24879		1.29	6.0E-01	5803136	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
12469	24855	30709	2.49	6.0E-01	9055303	NT	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA
12499	24810		6.92	6.0E-01	BE157617.1	EST_HUMAN	RC1-HT0375-030500-015-c03 HT0375 Homo sapiens cDNA
1038	13648	26160	1.09	5.9E-01	U32701.1	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
1447	14039	26588	1.06	5.9E-01	6680232	NT	Mus musculus 3-hydroxy-3-methylglutaryl-Coenzyme A lyase (Hmgcl), mRNA
3308	15919	28395	5.12	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3308	15919	28396	5.12	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4304	16890		4.32	5.9E-01	AF162756.1	NT	Rattus norvegicus cenexin 2 mRNA, partial cds
6591	19188	31991	1.48	5.9E-01	AF065440.2	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
7310	19838	32696	5.58	5.9E-01	AB023486.1	NT	Homo sapiens gene for histamine H2 receptor, promoter region and complete cds
7941	20483	33395	0.57	5.9E-01	D90911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1718643
9482	21987	34943	0.93	5.9E-01	AF063204.2	NT	Chlamydia trachomatis strain K/UW/31/Cx major outer membrane protein (omp1) gene, complete cds
9827	22325		0.68	5.9E-01	P06463	SWISSPROT	E6 PROTEIN
10091	22586	35579	1.15	5.9E-01	P55284	SWISSPROT	VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)
10551	23087	36102	3.24	5.9E-01	Q9X0I3	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
10557	23083	36105	1.75	5.9E-01	AF197944.1	NT	Xenopus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete cds
10840	23361	36376	3	5.9E-01	AW937175.1	EST_HUMAN	PM1-DT0041-190100-002-H03 DT0041 Homo sapiens cDNA
11073	23585	36626	2.25	5.9E-01	AF064626.1	NT	Mus spretus strain SPRET/EI CD48 antigen (Cd48) gene, partial cds
11810	24192	31030	1.92	5.9E-01	L42320.1	NT	Oryctolagus cuniculus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region
12053	24336		2.88	5.9E-01	AB017705.1	NT	Aspergillus oryzae pyrG gene for orotidine-5-phosphate decarboxylase, complete cds
12280	24483		7.56	5.9E-01	P34926	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
1982	14568	27092	1.8	5.8E-01	P40472	SWISSPROT	SIM1 PROTEIN
4056	16653	29119	1.22	5.8E-01	BF695738.1	EST_HUMAN	601852474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076131 5'
4612	17195	28841	3.73	5.8E-01	AB008077.1	NT	Vigna radiata mRNA for proton pyrophosphatase, complete cds
4914	17489		1.18	5.8E-01	AF110846.1	NT	Megascalia scalaris sex-lethal homolog (Megsxl) gene, partial cds, alternatively spliced products
5577	18208		0.75	5.8E-01	AE002152.1	NT	Ureaplasma urealyticum section 53 of 59 of the complete genome

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5722	18348	31051	2.52	5.8E-01	Q10699	SWISSPROT	POTENTIAL 5'-3' EXONUCLEASE
6331	18937	31713	2.37	5.8E-01	D78659.1	EST_HUMAN	HUM500E08B Human placenta polyA+ (T Fujiwara) Homo sapiens cDNA clone GEN-500E06 5'
6454	19055	31840	0.71	5.8E-01	D50601.1	NT	Shigella sonnei DNA for 26 ORFs, complete cds
6903	19637		2.47	5.8E-01	S65091.1	NT	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
7628	20370		2.57	5.8E-01	H41571.1	EST_HUMAN	yr91b03.s1 Soares adult brain N2b5HB65Y Homo sapiens cDNA clone IMAGE:175757 3' similar to
8031	20573	33477	0.66	5.8E-01	A1280051.1	EST_HUMAN	gb-S78187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN);
8031	20573	33478	0.66	5.8E-01	A1280051.1	EST_HUMAN	qh85d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8131	20672	33582	2.34	5.8E-01	P14328	SWISSPROT	qh85d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8131	20672	33583	2.34	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP96
8223	21362	34287	9.48	5.8E-01	AJ270774.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 6-11
8802	21440	34363	0.88	5.8E-01	Q27368	SWISSPROT	TRANSCRIPTION FACTOR E2F
8903	21441	34364	0.59	5.8E-01	Q20471	SWISSPROT	PUTATIVE CASEIN KINASE I F46F2.2 IN CHROMOSOME X
9514	22014		0.89	5.8E-01	BF031606.1	EST_HUMAN	60155777F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827288 5'
10869	23390	38405	9.44	5.8E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10915	23434		3.66	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284403 5'
11021	23535		2.04	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4284403 5'
3079	15684		0.66	5.7E-01	6755253	NT	Mus musculus plasmacytoma variant translocation 1 (Pvt1), mRNA
3260	15872	28352	1.58	5.7E-01	Q9WJT2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVOLIKE 1 (MOV01) (MOV01A)
3552	16156		2.63	5.7E-01	AB033503.1	NT	Populus euphratica peacs-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
3973	16571	28041	3.09	5.7E-01	AF011581.1	NT	Homo sapiens T cell receptor beta chain (BV6S7*2-BJ1S1) mRNA, partial cds
6496	19097	31881	3.67	5.7E-01	BF035413.1	EST_HUMAN	601454962F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858590 5'
6812	19403	32219	0.72	5.7E-01	AA194201.1	EST_HUMAN	z738c06.r1 Soares_NHMPJ_S1 Homo sapiens cDNA clone IMAGE:665674 5'
6945	18053	30478	1.28	5.7E-01	AL111440.1	NT	Borhys chinese strain T4 cDNA library under conditions of nitrogen deprivation
7741	20249	33142	1.97	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR)(P5C REDUCTASE)
7911	20453		0.57	5.7E-01	AJ251835.1	NT	Mus musculus Kcnq1, Ltpc5, Mash2, Tapa-1, Tssc6 and Tssc6 genes, alternative transcripts
9715	22213	35186	1.17	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
9715	22213	35187	1.17	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10468	22662	35673	0.86	5.7E-01	BF540962.1	EST_HUMAN	602067712F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4066610 5'
3410	16019	28498	1	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3410	16019	28499	1	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
4324	16910	29351	0.69	5.6E-01	D83135.1	NT	Chicken TGF gene, exon8, complete cds
8738	21277	34200	4.42	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKQFSF05 5'

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8738	21277	34201	4.42	5.6E-01	AY684703.1	EST_HUMAN	AV684703 GK/GK Homo sapiens cDNA clone GKCF5F05 5'
9287	21897	34844	1.11	5.6E-01	AB038782.1	NT	Homo sapiens MUC3A gene for intestinal mucin, partial cds
11658	24085		2.5	5.6E-01	BE888280.1	EST_HUMAN	601514007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915457 5'
11779	24166	36775	1.28	5.6E-01	AA493535.1	EST_HUMAN	ng75g10.s1 NCI_CGAP_P16 Homo sapiens cDNA clone IMAGE:940874 similar to contains element PTR7 repetitive element;
12156	18028	30480	3.31	5.6E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
12185	24419		2.56	5.6E-01	P50505	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
12618	24698		3.11	5.6E-01	BF573829.1	EST_HUMAN	602132029F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'
1253	13850	28387	1.13	5.5E-01	8393912	NT	Rattus norvegicus Prothymosin A carboxylase, beta polypeptide (Pccb), mRNA
2725	15280	27847	13.6	5.5E-01	P03341	SWISSPROT	GAG POLYPEPTIDE [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2725	15280	27848	13.6	5.5E-01	P03341	SWISSPROT	GAG POLYPEPTIDE [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2843	15559	28033	0.69	5.5E-01	5902085	NT	Homo sapiens superkiller viral-like activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
3102	15717		1.51	5.5E-01	H46219.1	EST_HUMAN	yo18a10.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:178268 3'
3271	15883	28365	2.68	5.5E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3755	18356	28825	0.97	5.5E-01	P48755	SWISSPROT	FOS-RELATED ANTIGEN-1
8386	20928	33846	0.68	5.5E-01	A1791766.1	EST_HUMAN	or82c01.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602336 5'
9682	22181		0.74	5.5E-01	U88415.1	NT	Crimean-Congo hemorrhagic fever virus strain SPU 415/85 nucleoprotein gene, complete cds
10279	22774	35763	0.84	5.5E-01	T05047.1	EST_HUMAN	EST02865 Fetal brain, Stratagene (cat#836208) Homo sapiens cDNA clone HFBCG35
151	12814	25301	12.97	5.4E-01	7857268	NT	Homo sapiens KIAA0929 protein Mix2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
151	12814	25302	12.97	5.4E-01	7857268	NT	Homo sapiens KIAA0929 protein Mix2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
611	13239	25713	1.6	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds; and unknown genes
611	13239	25714	1.6	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds; and unknown genes
1314	13908	28428	2.58	5.4E-01	AW696087.1	EST_HUMAN	QV4NN0040-070400-160-c04 NN0040 Homo sapiens cDNA
2154	14731		3.6	5.4E-01	AE002247.2	NT	Chlamydia pneumoniae AR39, section 74 of 84 of the complete genome
2296	14870	27446	2.18	5.4E-01	AJ276682.1	NT	Drosophila melanogaster mRNA for 15,15' beta carotene dioxygenase (beta-diox gene)
3984	16582	28053	0.82	5.4E-01	U07591.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5259	17822		1.04	5.4E-01	AW747972.1	EST_HUMAN	QV0-BT0041-061089-033-e02 BT0041 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5388	13239	25713	0.59	5.4E-01	AF232008.1	NT	<i>Pseudomonas syringae</i> pv. <i>tomato</i> strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
5388	13239	25714	0.59	5.4E-01	AF232008.1	NT	<i>Pseudomonas syringae</i> pv. <i>tomato</i> strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
5838	18462	31185	0.81	5.4E-01	AW842327.1	EST_HUMAN	PM2-CN0030-030200-003-c10 CN0030 Homo sapiens cDNA
6338	18944	31723	1.49	5.4E-01	AB025017.1	NT	<i>Rattus norvegicus</i> gene for TIS11, complete cds
7094	19665	32504	1.1	5.4E-01	BE96892.2	EST_HUMAN	601660276R1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3906080 3'
7374	19900	32782	0.75	5.4E-01	Z21619.1	NT	<i>S. cerevisiae</i> RIB3 gene encoding DBP synthase
7374	19900	32763	0.75	5.4E-01	Z21619.1	NT	<i>S. cerevisiae</i> RIB3 gene encoding DBP synthase
7378	19902	32786	1.47	5.4E-01	Q64428	SWISSPROT	MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) (INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE; LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE)
9801	22398	32786	1.88	5.4E-01	BF572536.1	EST_HUMAN	602076545F1 NIH_MGC 62 Homo sapiens cDNA clone IMAGE:4243690 5'
10957	23472	36497	3.25	5.4E-01	P38858	SWISSPROT	NITRATE REDUCTASE [NADPH] (NR)
11485	23934	37004	5.79	5.4E-01	Q60875	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11485	23934	37005	5.79	5.4E-01	Q60875	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN)
11586	18944	31723	2.42	5.4E-01	AB025017.1	NT	<i>Rattus norvegicus</i> gene for TIS11, complete cds
11725	24132		2.52	5.4E-01	A1858398.1	EST_HUMAN	w137g04 x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2427128 3' similar to gb:M13452 LAMIN A (HUMAN);
542	13173	25653	2.29	5.3E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK2W), RD, complement factor B (Bf), and complement component C2 (C2) genes >
2811	15363	27931	6.51	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2811	15363	27932	6.51	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3280	15691	28370	3.13	5.3E-01	AF087688.1	NT	Homo sapiens secreted C-type lectin precursor (LIS1L) gene, complete cds
4290	16876		1.39	5.3E-01	U39887.1	NT	<i>Mycoplasma genitalium</i> section 9 of 51 of the complete genome
5649	18277	30753	1.91	5.3E-01	A1820821.1	EST_HUMAN	zu42h12.y5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'
5649	18277	30754	1.91	5.3E-01	A1820821.1	EST_HUMAN	zu42h12.y5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'
5742	18368	31075	0.87	5.3E-01	AA193872.1	EST_HUMAN	zu42g09.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5'
5742	18368	31076	0.87	5.3E-01	AA193872.1	EST_HUMAN	zu42g09.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5'
5827	18451	31174	1.84	5.3E-01	BE645620.1	EST_HUMAN	7e73c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);
5827	18451	31175	1.84	5.3E-01	BE645620.1	EST_HUMAN	7e73c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783 PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8835	21374		1.83	5.3E-01	L01950.2	NT	Roridula gorgonias ribulose 1,5-bisphosphate carboxylase (rbcl) gene, partial cds; chloroplast gene for chloroplast product
8885	21423	34348	0.63	5.3E-01	BF433956.1	EST_HUMAN	7q71c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains element MER29 repetitive element
8885	21423	34349	0.63	5.3E-01	BF433956.1	EST_HUMAN	7q71c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains element MER29 repetitive element
10112	22607	35597	0.48	5.3E-01	AI954210.1	EST_HUMAN	wx94b02.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551275 3' similar to
11435	23885	36852	6.92	5.3E-01	BE566291.1	EST_HUMAN	SW:COXA_HUMAN P20874 CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR ;
11650	24881		4.22	5.3E-01	AA916053.1	EST_HUMAN	601339867F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682168 5'
849	13485	25973	19.16	5.2E-01	L20770.1	NT	cg30e05.s1 NCI_CGAP_B17 Homo sapiens cDNA clone IMAGE:1441376 3' similar to gb:J02811 APOLIPOPROTEIN D PRECURSOR (HUMAN);
1206	13808	26319	10.07	5.2E-01	Q8WV30	SWISSPROT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
1233	13832	26346	2.91	5.2E-01	AF224492.1	NT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5) (REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
1930	14514		4.11	5.2E-01	AL163285.2	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
2191	14767	27339	2.97	5.2E-01	AB018283.2	NT	Homo sapiens chromosome 21 segment HS21C085
3153	15787	28233	1.87	5.2E-01	U65942.1	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3274	15886		0.71	5.2E-01	D73443.1	NT	Chlamydomonas reinhardtii gene for isocitrate dehydrogenase, complete cds
3452	16059		1.74	5.2E-01	AL116780.1	NT	Azotobacter vinelandii gene for isocitrate dehydrogenase, complete cds
3492	16087	28572	2.49	5.2E-01	AA984165.1	EST_HUMAN	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
3694	16295		0.92	5.2E-01	AF020269.1	NT	am77g05.s1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504 3'
5161	17730		0.87	5.2E-01	7106444	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds
5314	17878		0.99	5.2E-01	AL163281.2	NT	Mus musculus vanilloid receptor-like protein 1 (Vhl1), mRNA
5834	18458	31179	0.97	5.2E-01	AA284261.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C081
9846	24795	35115	1.19	5.2E-01	X02218.1	NT	ze44409.T7 Soares_senescent_fibroblasts_NH9SF Homo sapiens cDNA clone IMAGE:325169 3'
9848	24795	35116	1.19	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
9845	22343	35325	0.64	5.2E-01	AA194518.1	EST_HUMAN	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
9940	22435	35411	1.65	5.2E-01	AF143952.2	NT	ze40509.r1 Stragene muscle 937208 Homo sapiens cDNA clone IMAGE:628793 5'
12590	24682		4.94	5.2E-01	P18516	SWISSPROT	Homo sapiens PELOTA (PELOTA) gene, complete cds
845	13268	25746	2.13	5.1E-01	M58509.1	NT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
876	13300	25781	3.98	5.1E-01	AIJ233944.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
							Polyangium vitellinum (strain PI vt1) 16S rRNA gene

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
676	13300	25782	3.98	5.1E-01	AJ233944.1	NT	Polyomavirus virelinum (strain PI vt1) 16S rRNA gene
1682	14284		0.88	5.1E-01	X87885.1	NT	R. norvegicus mRNA for mammalian fusca protein
2069	14649		11.33	5.1E-01	BF693095.1	EST_HUMAN	602139319F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4288117 5'
4151	16743	29197	4.61	5.1E-01	A1858495.1	EST_HUMAN	W39b12.x1 NCL_CGAP_UH Homo sapiens cDNA clone IMAGE:2427283 3'
4268	16852	29300	3.03	5.1E-01	P96380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
5229	17783		0.71	5.1E-01	BE081796.1	EST_HUMAN	IL2-BT0731-250400-077-G08 BT0731 Homo sapiens cDNA
6422	19025		0.79	5.1E-01	AV712326.1	EST_HUMAN	AV712326 DCA Homo sapiens cDNA clone DCAAF07 5'
6997	19495	32316	1.42	5.1E-01	R80873.1	EST_HUMAN	y64609.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148872 3'
8507	21046	33966	0.73	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-401 ST0023 Homo sapiens cDNA
8507	21046	33967	0.73	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-401 ST0023 Homo sapiens cDNA
9802	22102	35065	4.6	5.1E-01	J05412.1	NT	Human regenerating protein (reg) gene, complete cds
9805	22105	35068	3.4	5.1E-01	W22302.1	EST_HUMAN	65B1 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional
10065	22580	35555	0.95	5.1E-01	M94579.1	NT	Human carboxyl ester lipase (CEL) gene, complete cds
11874	24805		2.04	5.1E-01	BF030207.1	EST_HUMAN	601555863F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826767 5'
12129	24385		2.01	5.1E-01	BF439982.1	EST_HUMAN	nac511f10.x1 NCL_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3406218 3' similar to contains element TAR1 repetitive element
2180	14757	27326	1.4	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2180	14757	27327	1.4	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2189	14765	27335	5.46	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene
2189	14765	27336	5.48	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene
3740	16341	28809	5.58	5.0E-01	A001785.1	NT	Thermococcus maritima section 97 of 136 of the complete genome
3811	18410	28875	0.65	5.0E-01	U55574.1	NT	Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibody 363p.138, partial cds
3842	16540	29006	3.11	5.0E-01	AB033010.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
8467	21007		1.78	5.0E-01	M92304.1	NT	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds
8604	21143	34057	0.64	5.0E-01	BF107848.1	EST_HUMAN	601823850R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043485 3'
9379	20318	33219	3.1	5.0E-01	BF317212.1	EST_HUMAN	601903871F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136832 5'
9543	22043	35004	1.34	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE] (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9543	22043	35005	1.34	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE), AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
10291	22786		1.04	5.0E-01	BE869218.1	EST_HUMAN	601445024F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849436 5'
11815	24187		3.45	5.0E-01	AF029215.1	NT	Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds
12554	24656		2.38	5.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
12569	24688		4.27	5.0E-01	OT3981	SWISSPROT	NUCLEAR ENVELOPE PROTEIN OUT11
822	13439	25946	2.31	4.9E-01	BF571462.1	EST_HUMAN	602076649F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4243860 5'
1699	14292	28827	1.6	4.9E-01	AJ243955.1	NT	Xenopus laevis mRNA for c-Jun protein, 1878 BP
1949	14533	27089	1.35	4.9E-01	U40869.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds
5602	18231	30681	1.32	4.9E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR
6187	18797	31565	2.35	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
6187	18797	31566	2.35	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
7475	19997	32862	1.9	4.9E-01	AB040051.1	NT	Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
8920	21458		1.49	4.9E-01	BF209791.1	EST_HUMAN	601874984F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102503 5'
9115	21651	34592	0.96	4.9E-01	AW339805.1	EST_HUMAN	hc90c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2907266 3' similar to TR:O95714
9220	25125		2.2	4.9E-01	10846863	NT	O95714 HERC2.1
10220	22715	35706	0.74	4.9E-01	AF053980.1	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA
11704	24117		2.48	4.9E-01	AF176912.1	NT	Mus musculus adenyl cyclase 1 (Adcy1) cDNA, partial cds
12546	25081		5.73	4.9E-01	AA613562.1	EST_HUMAN	Homo sapiens neurotrophin-1/B-cell stimulating factor-3 gene, complete cds
12555	24657	30872	1.74	4.9E-01	AL163301.2	NT	ng22e11.s1 NCL CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144652 3'
12630	24708		1.36	4.9E-01	11431438	NT	Homo sapiens chromosome 21 segment HS21C101
3591	16195		1.05	4.8E-01	AA912842.1	EST_HUMAN	Homo sapiens eukaryotic translation initiation factor 4 gamma, 1 (EIF4G1), mRNA
4782	17011		0.62	4.8E-01	4504850	NT	cl32a09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1525144 3'
5698	18324	30827	8.6	4.8E-01	J02987.1	NT	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
6790	19381		4.22	4.8E-01	AA659878.1	EST_HUMAN	Saccharomyces cerevisiae sporulation protein (SPO11) gene required for meiotic recombination, complete cds
7357	19883		1.85	4.8E-01	5031650	NT	nu85f09.s1 NCL CGAP_Alt1 Homo sapiens cDNA clone IMAGE:1217513
7662	20174	33061	0.87	4.8E-01	AL163209.2	NT	Homo sapiens reproduction 8 (DS22298E) mRNA
7738	20246	33138	3.72	4.8E-01	AL161492.2	NT	Homo sapiens chromosome 21 segment HS21C009
7738	20246	33139	3.72	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7846	20388	33291	1.36	4.8E-01	AB20744.1	EST_HUMAN	W7710.y6 Soares breast 2NhbIBst Homo sapiens cDNA clone IMAGE:154795 5' similar to contains element MER6 repetitive element :
9169	21746		1.13	4.8E-01	BE155148.1	EST_HUMAN	PM1-H10350-201299-004-504 HT0350 Homo sapiens cDNA
9921	22417		0.58	4.8E-01	BF568833.1	EST_HUMAN	602184267F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300048 5'
10607	23141		2.02	4.8E-01	X83502.1	NT	S cerevisiae ORFs from chromosome X
11786	24170		1.29	4.8E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
12016	24842		3.04	4.8E-01	AF227565.1	NT	Trypanosoma cruzi transposon VIP II SIRE repeat region
12846	24896		3.36	4.8E-01	AJ132984.1	NT	Chlamydomonas reinhardtii cop gene, exons 1-8
6638	19234	32036	8.72	4.7E-01	BF211713.1	EST_HUMAN	601893880F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096387 5'
7107	19447	32263	0.78	4.7E-01	A1204374.1	EST_HUMAN	q172a09.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1755544 3'
7806	20349	33257	0.52	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
7806	20349	33258	0.52	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
9005	21542	34473	0.5	4.7E-01	6981501	NT	Rattus norvegicus Spermine binding protein (Sbp), mRNA
10467	22961	35972	0.79	4.7E-01	AW087791.1	EST_HUMAN	x659e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581580 3'
10727	23253		4.94	4.7E-01	AF102673.1	NT	Influenza A virus isolate h151697 hemagglutinin (HA) gene, partial cds
10963	23478	36503	2.19	4.7E-01	U41089.1	NT	Human collagen alpha2(XI)(COL11A2) gene, exons 6 through 16, and partial cds
11183	23670	36715	11.61	4.7E-01	BF529658.1	EST_HUMAN	602043889F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4181303 5'
11254	23784	36840	2.89	4.7E-01	AW889448.1	EST_HUMAN	RC6-NT0029-240400-011-E08 NT0028 Homo sapiens cDNA
11904	24243		1.92	4.7E-01	BE887683.1	EST_HUMAN	601511333F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912488 5'
12036	24325		1.33	4.7E-01	AW341561.1	EST_HUMAN	hd11c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2809198 3'
12666	24736		1.38	4.7E-01	AP000007.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1485001-1738505 nt. position (777)
3797	16397	28862	2.23	4.6E-01	AW818638.1	EST_HUMAN	RC1-ST0278-040400-018-506 ST0278 Homo sapiens cDNA
3806	16406	28870	1.68	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
3806	16406	28871	1.68	4.6E-01	BF693300.1	EST_HUMAN	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5323	17885		1.03	4.6E-01	M11267.1	NT	Bovine steroid 21-hydroxylase gene (P-450-c21) gene, complete cds
5429	17886	30590	22.08	4.6E-01	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
							AMILORIDE-SENSITIVE SODIUM CHANNEL GAMMA-SUBUNIT (EPITHELIAL NA+ CHANNEL GAMMA SUBUNIT) (SCN5G) (GAMMA NACH)
5440	17995	30400	1.37	4.6E-01	P51170	SWISSPROT	
5612	18241	30690	1.12	4.6E-01	BF313593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5612	18241	30691	1.12	4.6E-01	BF313593.1	EST_HUMAN	601900234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5663	18280	30768	3.27	4.6E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5663	18280	30769	3.27	4.6E-01	Q90643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5735	18361	31067	2.39	4.6E-01	BE734781.1	EST_HUMAN	601568755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5748	18374	31082	4.22	4.6E-01	A1247678.1	EST_HUMAN	qh59h02.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1848011 3' similar to TR:O15338 O15338 BUTYROPHILIN.;
5748	18374	31083	4.22	4.6E-01	A1247678.1	EST_HUMAN	qh59h02.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1848011 3' similar to TR:O15338 O15338 BUTYROPHILIN.;
5768	18382	31084	1.4	4.6E-01	P20050	SWISSPROT	MEIOSIS SPECIFIC PROTEIN HOP1
5828	18452		1.05	4.6E-01	AF212124.1	NT	Anolis schwartzi cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product
5807	18528		0.86	4.6E-01	BE817247.1	EST_HUMAN	PMO-BN0260-120500-001-F07 BN0260 Homo sapiens cDNA
6058	18675	31417	0.75	4.6E-01	D26215.1	NT	Unidentified soil bacteria 16S rRNA gene encoding 16S ribosomal RNA
8404	19007	31788	1.05	4.6E-01	AE000894.1	NT	Methanobacterium thermoautotrophicum from bases 1165751 to 1176238 (section 100 of 148) of the complete genome
6865	19599	32429	1.36	4.6E-01	U82332.1	NT	Emricella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6865	19599	32430	1.36	4.6E-01	U82332.1	NT	Emricella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7712	20221	33108	0.86	4.6E-01	AA486577.1	EST_HUMAN	hh04h05.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943353 similar to contains Alu repetitive element; contains element L1 repetitive element;
8262	20803	33721	13.23	4.6E-01	BF697398.1	EST_HUMAN	802130953F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287828 5'
9225	21741	34684	1.04	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9225	21741	34685	1.04	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
9583	22083	35048	0.55	4.6E-01	AF162283.1	NT	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product
9583	22083	35047	0.55	4.6E-01	AF162283.1	NT	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product
9888	22383	35358	2.63	4.6E-01	A1815634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370768 3'
9888	22383	35359	2.63	4.6E-01	A1815634.1	EST_HUMAN	wg73e12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370768 3'
10870	23391		3.09	4.6E-01	P98163	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (VL)
10878	23400	36416	4.13	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
10879	23400	36417	4.13	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11346	23044	36054	5.52	4.6E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
11346	23044	36055	5.52	4.6E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
12854	24726		1.26	4.6E-01	M22380.1	NT	Rat plasma proteinase inhibitor alpha-1-inhibitor III group 3 variants 6J, 12J, 13J, and 17J mRNA, partial cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1954	14538	27094	1.69	4.5E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 228 of the complete chromosome 1
1954	14538	27095	1.69	4.5E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 228 of the complete chromosome 1
2895	15512	27982	4.77	4.5E-01	AA877086.1	EST_HUMAN	z55d02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:464179 3'
3346	15956	28431	0.64	4.5E-01	AW083761.1	EST_HUMAN	xc25c06.x1 NCL_CGAP_Co19 Homo sapiens cDNA clone IMAGE:2585290 3' similar to gb:U07807
3346	15956	28432	0.64	4.5E-01	AW083761.1	EST_HUMAN	xc25c06.x1 NCL_CGAP_Co19 Homo sapiens cDNA clone IMAGE:2585290 3' similar to gb:U07807
3359	15967	28444	5.18	4.5E-01	Q05793	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
3424	16032	28512	1.15	4.5E-01	AF126378.1	NT	PRECURSOR (HSPG) (PERLECAN) (PLC)
4100	16694		1.35	4.5E-01	Q28247	SWISSPROT	Mus musculus DNA polymerase epsilon catalytic subunit (Pole) gene, exons 2 through 12
4149	16741	29195	0.73	4.5E-01	AI708908.1	EST_HUMAN	COLLAGEN ALPHA 5(IV) CHAIN
4255	18015		4.04	4.5E-01	AW873495.1	EST_HUMAN	as06609.x1 Barstead aorta HPLRBB Homo sapiens cDNA clone IMAGE:2353480 3'
5078	17651	30092	1.16	4.5E-01	BE683445.2	EST_HUMAN	hs00g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
5427	17984		26.74	4.5E-01	AF060195.1	NT	60165722R1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866023 3'
5737	18363	31070	1.37	4.5E-01	AW608814.1	EST_HUMAN	Mus musculus proteasome regulator PA28 beta subunit gene, complete cds
6719	19313		1.36	4.5E-01	Q00956	SWISSPROT	QV2-PT0012-140100-031-c09 PT0012 Homo sapiens cDNA
7443	19967	32834	1.69	4.5E-01	M37036.1	NT	COAT PROTEIN
7604	20117	32993	2.53	4.5E-01	AI858849.1	EST_HUMAN	Rat nuclear proteins B23.1 and B23.2
8249	20780		0.97	4.5E-01	M32661.1	NT	W32602.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2426618 3' similar to TR:Q92923 Q92923
8342	20883	33804	4.02	4.5E-01	AI648596.1	EST_HUMAN	SWISNF COMPLEX 170 KDA SUBUNIT.1
							D melanogaster Shaw2 protein mRNA, complete cds
							tz56g1.x1 NCL_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2282644 3'
8494	21033	33954	0.69	4.5E-01	Q52728	SWISSPROT	POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(3-HYDROXYBUTYRATE) POLYMERASE) (PHB POLYMERASE) (PHB SYNTHASE) (POLY(3-HYDROXYALKANOATE) POLYMERASE) (PHA POLYMERASE) (PHA SYNTHASE) (POLYHYDROXYALKANOIC ACID SYNTHASE)
8716	21255		1.74	4.5E-01	11444786	NT	Homo sapiens hypothetical protein DKFZp547G183 [DKFZp547G183]. mRNA
8928	21467	34385	0.69	4.5E-01	AE000218.1	NT	Escherichia coli K-12 MG1655 section 108 of 400 of the complete genome
9853	22351		1.02	4.5E-01	9630816	NT	Bombyx mori nuclear polyhedrosis virus, complete genome
10389	22883	35877	23.95	4.5E-01	M86006.1	EST_HUMAN	EST102531 Fetal brain, Stratagene (cat#836206) Homo sapiens cDNA clone HFBCY17
10389	22883	35878	23.95	4.5E-01	M86006.1	EST_HUMAN	EST102531 Fetal brain, Stratagene (cat#836206) Homo sapiens cDNA clone HFBCY17
10744	23268	36285	3.01	4.5E-01	AW591271.1	EST_HUMAN	xc14h01.x1 NCL_CGAP_U13 Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW:INT6_MOUSE
11131	23639		1.9	4.5E-01	AV719382.1	EST_HUMAN	Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6. [1].
							AV719382 GLC Homo sapiens cDNA clone GLCCED12 5'

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11376	23826	38890	1.88	4.5E-01	BE068472.1	EST_HUMAN	RC3-BT0333-160300-016-a03 BT0333 Homo sapiens cDNA
11671	25070		3.3	4.5E-01	BE871461.1	EST_HUMAN	601449201F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852961 5'
12370	24540		2.13	4.5E-01	BF337531.1	EST_HUMAN	602035275F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4183280 5'
12442	24578		6.25	4.5E-01	11422099	NT	Homo sapiens testis-specific kinase 2 (TESK2), mRNA
2081	14662		1.39	4.4E-01	6680503	NT	Mus musculus integral membrane-associated protein 1 (Imap1), mRNA
2432	14999	27572	3.26	4.4E-01	P49765	SWISSPROT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3357	15965	28442	1.27	4.4E-01	AF058790.1	NT	Rattus norvegicus SmGAP-b mRNA, complete cds
3357	15965	28443	1.27	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3361	15968	28446	2.31	4.4E-01	BF056726.1	EST_HUMAN	7191402.Y1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3393795 5'
4318	18904		1.28	4.4E-01	BE378707.1	EST_HUMAN	601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609393 5'
5134	17706		2.07	4.4E-01	BE141396.1	EST_HUMAN	MRO-HT0078-131299-007-g05 HT0078 Homo sapiens cDNA
5277	17839	30265	0.94	4.4E-01	U61154.1	NT	Buzura suppressaria nucleopolydnavirus ecdysteroid UDP-glucosyltransferase (egt) gene, complete cds
5417	17974		0.9	4.4E-01	AW814885.1	EST_HUMAN	MR1-ST0208-120400-022-g07 ST0208 Homo sapiens cDNA
5613	18242	30692	4.06	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5613	18242	30693	4.06	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5687	18489	31215	1.72	4.4E-01	S65019.1	NT	mucin [rats, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 390 nt]
5883	18505	31231	1.9	4.4E-01	AV720408.1	EST_HUMAN	AV720408 GLC Homo sapiens cDNA clone GLCCSC12 5'
6108	18724	31476	1.53	4.4E-01	AI198413.1	EST_HUMAN	q162h11.x1 NCI_CGAP_Br25 Homo sapiens cDNA clone IMAGE:1861125 3' similar to TR:Q29168 Q29168
6108	18724	31477	1.53	4.4E-01	AI198413.1	EST_HUMAN	UNKNOWN PROTEIN ;
6387	18960	31771	1.69	4.4E-01	AW080795.1	EST_HUMAN	UNKNOWN PROTEIN ;
6470	19071		1.02	4.4E-01	AA778132.1	EST_HUMAN	xc27e08.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2585510 3' similar to TR:O85154 O85154
7429	19953	32818	0.89	4.4E-01	AE000371.1	NT	AFLATOXIN B1-ALDEHYDE REDUCTASE ;
7782	20325		10.05	4.4E-01	Z11679.1	NT	ae85d11.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970865 3' similar to gb:M16038
8688	21237	34160	1.01	4.4E-01	AA056427.1	EST_HUMAN	TYROSINE-PROTEIN KINASE LYN (HUMAN);
9078	21614	34549	0.76	4.4E-01	AF112540.1	NT	Helicobacter pylori 26695 section 49 of 134 of the complete genome
9111	21647	34587	0.56	4.4E-01	AW612578.1	EST_HUMAN	S tuberosum mRNA for induced stolon tip protein (partial)
9214	21731	34674	1.13	4.4E-01	O62836	SWISSPROT	z169a03.s1 Stralagene colon (#837204) Homo sapiens cDNA clone IMAGE:509836 3'
							HIV-1 isolate 08107v6 from USA, envelope glycoprotein (env) gene, partial cds
							SW_MSH6_HUMAN P92701 DNA MISMATCH REPAIR PROTEIN MSH6 ;
							ZINC FINGER X-CHROMOSOMAL PROTEIN

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9872	22369	35347	1.89	4.4E-01	AI268650.1	EST_HUMAN	gc39709.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910921 3'
9873	22370		2.12	4.4E-01	P28922	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
10009	22504	35495	4.51	4.4E-01	P35590	SWISSPROT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
10276	22771	35759	1.43	4.4E-01	S76404.1	NT	beta-HKA-H1-K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
10276	22771	35760	1.43	4.4E-01	S76404.1	NT	beta-HKA-H1-K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
11939	24271	31016	4.68	4.4E-01	6677874	NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
11952	25000		14.98	4.4E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
12517	24635		1.5	4.4E-01	P54725	SWISSPROT	UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG A (HHR23A)
436	13069	25594	1.77	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
436	13069	25565	1.77	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
3096	15711	28182	0.91	4.3E-01	AW999477.1	EST_HUMAN	MRO-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
4231	18819	29268	1.21	4.3E-01	J00306.1	NT	Human somatostatin 1 gene and flanks
4495	13069	25564	3.96	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
4495	13069	25565	3.96	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
5567	18198	30645	0.76	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5567	18198	30646	0.76	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
6049	18688	31407	1.34	4.3E-01	BE181655.1	EST_HUMAN	QV1-HT0638-070500-191-d08 HT0638 Homo sapiens cDNA
6065	18682	31424	2.06	4.3E-01	AF179825.1	NT	Salimiri sclerous olfactory receptor (SSC186) gene, partial cds
6809	19400	32215	4.28	4.3E-01	AJ001678.1	NT	Coturnix coturnix japonica fnG gene
6849	19526		0.78	4.3E-01	O33367	SWISSPROT	DNA GYRASE SUBUNIT B
7456	19980		1.76	4.3E-01	BF348001.1	EST_HUMAN	602023134F1 NCL_CGAP_Bri67 Homo sapiens cDNA clone IMAGE:4158296 5'
8368	20906		2.66	4.3E-01	U97040.1	NT	Methanococcus voltae flagellar-related protein C-1 (flaC-fla) genes, complete cds
9179	21758	34702	0.7	4.3E-01	Y14604.1	NT	Erwinia amylovora rcsV gene
9642	22142	35109	2.63	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968554 5'
9642	22142	35110	2.63	4.3E-01	AW630048.1	EST_HUMAN	hh74e10.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968554 5'
10128	22823	35614	0.57	4.3E-01	AW170559.1	EST_HUMAN	xn63e05.x1 Soares_NHCc cervical_tumor Homo sapiens cDNA clone IMAGE:2698400 3' similar to
10811	19616	32451	2.52	4.3E-01	AF075629.1	NT	TR:O00189 O00189 MU-ADAPTIN-RELATED PROTEIN 2 ;
11588	24031	37101	1.54	4.3E-01	AI874332.1	EST_HUMAN	Equus caballus microsatellite LEX027
11632	18198	30645	1.55	4.3E-01	P48634	SWISSPROT	tb44d04.x1 NCL_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2293351 3'
11632	18198	30646	1.55	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
12616	24696		2.81	4.3E-01	AJ003022.1	NT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
1402	15440	26524	1.39	4.2E-01	Q39102	SWISSPROT	Streptomyces coelicolor whiH gene
1991	14573		1.04	4.2E-01	AA761653.1	EST_HUMAN	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
							n224a09.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288698 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2068	14648		1.37	4.2E-01	AF268325.1	NT	Plasmodium falciparum multidrug resistance protein Pgh1 gene, complete cds
3669	16270	28738	4.91	4.2E-01	AE003947.1	NT	Xyella fastidiosa, section 93 of 229 of the complete genome
3699	16300	28768	1	4.2E-01	AI280338.1	EST_HUMAN	q194b01.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1879845 3'
3773	18014		0.6	4.2E-01	N81203.1	EST_HUMAN	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE1-K similar to R07879, Z40498
3948	16546	29014	0.73	4.2E-01	AW835527.1	EST_HUMAN	QV0-L T0015-180200-127-H01 LT0015 Homo sapiens cDNA
4054	16651	29118	0.98	4.2E-01	Q04886	SWISSPROT	SOX-8 PROTEIN
4807	17365	29835	4.3	4.2E-01	AA534088.1	EST_HUMAN	η99h01.s1 NCL CGAP_P110 Homo sapiens cDNA clone IMAGE:997777 similar to gb.M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
4895	17470	29928	4.04	4.2E-01	R13487.1	EST_HUMAN	y77601.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28278 5'
5232	17796		3.77	4.2E-01	U50871.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
5891	18514	31241	1.52	4.2E-01	BF242053.1	EST_HUMAN	601879721F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4103493 5'
5953	18575	31309	2.16	4.2E-01	AW864162.1	EST_HUMAN	RC3-CT0254-060400-029-g04 CT0254 Homo sapiens cDNA
6352	18957	31736	1.06	4.2E-01	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
7031	19565	32392	10.29	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7031	19565	32393	10.29	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7082	24778	32492	1.97	4.2E-01	S82504.1	NT	Brcal=breast cancer gene [Rats, WF, spleen, Genomic, 419 nt, segment 2 of 2]
7150	19693	32524	5.81	4.2E-01	AL161547.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
7834	20476	33385	2.81	4.2E-01	AW957448.1	EST_HUMAN	EST369413 IMAGE resequences, IMAGE Homo sapiens cDNA
7834	20476	33386	2.81	4.2E-01	AW957448.1	EST_HUMAN	EST369413 IMAGE resequences, IMAGE Homo sapiens cDNA
8148	20689	33602	0.55	4.2E-01	4758039	NT	Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA
9235	21761	34708	0.52	4.2E-01	U57431.1	NT	Human cytomegalovirus early phosphoprotein p50 mRNA, complete cds
9235	21761	34707	0.52	4.2E-01	U57431.1	NT	Human cytomegalovirus early phosphoprotein p50 mRNA, complete cds
9890	22377		0.81	4.2E-01	AA705007.1	EST_HUMAN	z95f01.s1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462849 3'
10093	22578	35571	0.5	4.2E-01	AF181854.1	NT	Lassa virus strain 803213 glycoprotein precursor and nucleoprotein genes, complete cds
10390	22894	35879	1.35	4.2E-01	AW883666.1	EST_HUMAN	MR3-SN0010-280300-103-H07 SN0010 Homo sapiens cDNA
10921	23440	36481	3.89	4.2E-01	AB023489.1	NT	Oryza latipes OIGC7 mRNA for membrane guanylyl cyclase, complete cds
11273	23728	36780	2.85	4.2E-01	BE966485.2	EST_HUMAN	801660352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906085 3'
12581	24681		1.49	4.2E-01	AV731815.1	EST_HUMAN	AV731815 HTF Homo sapiens cDNA clone HTFBHH05 5'
1133	13736	26245	1.59	4.1E-01	A1805481.1	EST_HUMAN	RC-BT091-210199-142 BT091 Homo sapiens cDNA
1142	13745	26254	1.54	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1142	13745	26255	1.54	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
2735	15290	27858	1.59	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2867	15582	28091	2.11	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2967	15982	28062	2.11	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3342	15952	28428	0.86	4.1E-01	AA908344.1	EST_HUMAN	q94b08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3'
3839	16438	28899	0.58	4.1E-01	AW961292.1	EST_HUMAN	EST373364 MAGE resequences, MAGG Homo sapiens cDNA
3839	16438	28900	0.58	4.1E-01	AW961292.1	EST_HUMAN	EST373364 MAGE resequences, MAGG Homo sapiens cDNA
4361	16948	29390	2.82	4.1E-01	AJ249207.1	NT	Rhodococcus sp. AD45 isoG, isoH, isoI, isoA, isoB, isoE and isoF genes
4393	16979		0.76	4.1E-01	AA909257.1	EST_HUMAN	on33d02.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1542819 3'
4774	17355	29807	1.31	4.1E-01	AV747880.1	EST_HUMAN	AV747880 NPC Homo sapiens cDNA clone NPCBDF10 5'
6141	18755	31513	3.97	4.1E-01	BF681393.1	EST_HUMAN	602156590F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297319 5'
7480	19883	32848	2.74	4.1E-01	U87535.1	NT	Methanococcus jannaschii section 77 of 150 of the complete genome
7979	20521	33427	1.31	4.1E-01	BF574804.1	EST_HUMAN	602133261F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288238 5'
9019	21556	34484	1.28	4.1E-01	8755521	NT	Mus musculus signaling intermediate in Toll pathway-evolutionarily conserved (Sitbec-pending), mRNA
9484	21941		0.61	4.1E-01	AF160597.1	NT	Vesalius gymnocaudus Vgym580 cytochrome b (cyb) gene, complete cds; mitochondrial gene for mitochondrial product
10184	22659		1.26	4.1E-01	AL139076.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 3/8
10310	22804	35798	0.79	4.1E-01	AV649579.1	EST_HUMAN	AV649579 GLC Homo sapiens cDNA clone GLOBVD12 3'
10401	22895	35890	0.51	4.1E-01	P18584	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)
10401	22895	35891	0.51	4.1E-01	P18584	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)
10471	22965		2.29	4.1E-01	BF349382.1	EST_HUMAN	GM2-HT0137-200999-010-408 HT0137 Homo sapiens cDNA
10719	23247	36262	45.22	4.1E-01	X58700.1	NT	Zea mays ZMPMS2 gene for 19 kDa zein protein
11270	23008	36015	3.57	4.1E-01	Q09470	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUK1) (HBK1)
12290	25049		2.6	4.1E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1477	15408		4.55	4.0E-01	AW847123.1	EST_HUMAN	RC2-CT0201-290999-012-410 CT0201 Homo sapiens cDNA
1394	13978	26505	1.51	4.0E-01	AF203478.1	NT	Laqueus rubellus mitochondrion, complete genome
1592	14124		4.1	4.0E-01	6879258	NT	Drosophila melanogaster Dalmatian (dmt) mRNA, complete cds
2049	15456	27200	1.22	4.0E-01	Z96933.1	NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
2049	15456	27201	1.22	4.0E-01	Z96933.1	NT	Ascaris lumbricoides msc2 gene
2204	14780	27352	17.82	4.0E-01	AE001831.1	NT	Ascaris lumbricoides msc2 gene
2204	14780	27353	17.82	4.0E-01	AE001831.1	NT	Deinococcus radiodurans R1 section 88 of 229 of the complete chromosome 1
2831	12811	25299	1.45	4.0E-01	6878490	NT	Deinococcus radiodurans R1 section 88 of 229 of the complete chromosome 1
2995	15611	28090	1.23	4.0E-01	AL163280.2	NT	Mus musculus ubiquitin-protein ligase e3 component n-recogin (Ubr1), mRNA
2995	15611	28091	1.23	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3758	16359	28829	2.17	4.0E-01	AF068903.1	NT	Streptococcus pneumoniae Y1C (y1C), Y1D (y1D), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3899	16498	28960	3.04	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3899	16498	28961	3.04	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
4942	17517		8.41	4.0E-01	Q31849	SWISSPROT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
6069	18898	31429	1.18	4.0E-01	AW970610.1	EST_HUMAN	EST382691 MAGE resequences, MAGK Homo sapiens cDNA
6967	19165	31981	0.87	4.0E-01	P27285	SWISSPROT	STRUCTURAL POLYPROTEIN (P130) [CONTAINS: COAT PROTEIN C; SPIKE GLYCOPROTEINS E3, E2 AND E1; 6 KD PEPTIDE]
7777	20286	33183	0.72	4.0E-01	P27546	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 4
7869	20411	33317	0.46	4.0E-01	BF082634.1	EST_HUMAN	MR4-TN0110-180900-202-g02 TN0110 Homo sapiens cDNA
7954	20498	33408	0.99	4.0E-01	AB016625.1	NT	Homo sapiens OCTN2 gene, complete cds
8936	21474	34394	0.98	4.0E-01	AA323289.1	EST_HUMAN	EST26066 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
11443	23893		1.65	4.0E-01	BF030282.1	EST_HUMAN	601558283F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE:3828092 5'
11568	24015		3.52	4.0E-01	L76080.1	NT	Synechocystis sp. PCC 9413 transposase gene, complete cds
11958	24901		2.5	4.0E-01	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
12518	24636		1.42	4.0E-01	P36049	SWISSPROT	HYPOTHETICAL 49.7 KD PROTEIN IN GIN2-STE3 INTERGENIC REGION
1420	14013	26543	1.98	3.9E-01	AF206618.1	NT	Gonilla gorilla carboxy-ester lipase (CEL) gene, complete cds
2668	15226	27798	3.8	3.9E-01	AB033019.1	NT	Homo sapiens mRNA for KIAA1193 protein, partial cds
2730	15285	27851	3.79	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
2730	15285	27852	3.79	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
3131	15745	28214	3.95	3.9E-01	AJ258896.1	NT	Sinorhizobium meliloti egl, syb2, cya3 genes and orf3
4153	16745	29189	1.49	3.9E-01	BF592611.1	EST_HUMAN	7161d01.x1 NCI_CGAP_B118 Homo sapiens cDNA clone IMAGE:3339169 3'
5130	17702	30136	1.86	3.9E-01	BE728867.1	EST_HUMAN	601563948F1 NIH_MGC 20 Homo sapiens cDNA clone IMAGE:3833698 5'
6080	18706	31454	6.44	3.9E-01	BF208036.1	EST_HUMAN	601862362F1 NIH_MGC 53 Homo sapiens cDNA clone IMAGE:4082055 5'
6426	19029	31812	0.68	3.9E-01	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
7896	20438	33343	0.78	3.9E-01	U79415.1	NT	Homo sapiens prepro dipeptidyl peptidase 1 (DPP-1) gene, complete cds
8765	21334	34259	0.73	3.9E-01	AW177011.1	EST_HUMAN	CM8-CT0105-170899-004-b08 CT0105 Homo sapiens cDNA
8804	21343		0.7	3.9E-01	BF348634.1	EST_HUMAN	602019944F1 NCI_CGAP_B187 Homo sapiens cDNA clone IMAGE:4155322 5'
9161	21696	34640	1.24	3.9E-01	AW185888.1	EST_HUMAN	xn8d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701351 3' similar to TR:O94821 O94821 KIAA0713 PROTEIN :

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9464	21989	34945	1.42	3.9E-01	AI937337.1	EST_HUMAN	wp7602.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2467658 3' similar to SW_RFX5 HUMAN P4382 BINDING REGULATORY FACTOR ;
9792	22290	35274	3.68	3.9E-01	M18879.1	NT	Human diaphanin 27 gene, exons 10 and 11, and L1 and Alu repeats
9856	22354		0.5	3.9E-01	11465620	NT	Porphyra purpurea mitochondrion, complete genome
10071	22566	35561	0.69	3.9E-01	D86722.1	NT	Nicotiana tabacum mRNA for TATA binding protein (TBP), complete cds
10492	22986	35953	0.46	3.9E-01	M18440.1	NT	Human beta-B2-crystallin (B2-1) gene, exon 4, partial cds
10700	23229		1.82	3.9E-01	AV695974.1	EST_HUMAN	AV695974 GKC Homo sapiens cDNA clone GKCBCQ11 5'
11729	24977		3.42	3.9E-01	AF304354.1	NT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
11854	24214		1.42	3.9E-01	Q61670	SWISSPROT	HOMEOBOX PROTEIN HLX1
11930	24285	31015	1.56	3.9E-01	AE001811.1	NT	Thermotoga maritima section 123 of 136 of the complete genome
12389	24551		1.37	3.9E-01	11433335	NT	Homo sapiens hypothetical protein FLJ10583 (FLJ10583), mRNA
171	12834		19.28	3.8E-01	7019488	NT	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
531	13162		3.11	3.8E-01	AB028291.1	NT	Mus musculus pcm-1 mRNA for pericentriolar material-1, complete cds
1911	14406		0.99	3.8E-01	AE003870.1	NT	Xyella fastidiosa, section 16 of 229 of the complete genome
2605	15167	27734	1.89	3.8E-01	AF214117.1	NT	Arabidopsis thaliana putative c-myc-like transcription factor (MYB3R-3) mRNA, complete cds
2661	15473	27781	3.94	3.8E-01	6678002	NT	Mus musculus solute carrier family 1, member 6 (Slc1a6), mRNA
3034	15650		0.89	3.8E-01	AJ251057.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 98SE-MP1213)
3084	15699	28173	2.2	3.8E-01	AF043383.1	NT	Pleurocetes americanus aminopeptidase N (ampN) gene, partial cds
3530	16135	28615	9.83	3.8E-01	AL161518.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
3592	16196		0.59	3.8E-01	AI807219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3609	16196		0.75	3.8E-01	AI807219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3820	16420	28882	0.94	3.8E-01	BE154080.1	EST_HUMAN	PIM0-HT0339-200400-010-G01 HT0339 Homo sapiens cDNA
3989	16587	28058	0.8	3.8E-01	6754095	NT	Mus musculus general transcription factor III (GTF2), mRNA
4138	16730	29183	0.69	3.8E-01	AJ271381.2	NT	Takifugu rubripes wnt2 (partial), frank1, cfr and frank2 (partial) genes
5271	17833	30259	0.96	3.8E-01	BE544653.1	EST_HUMAN	601074110F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3460154 5'
							yr68a11.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:210428 5' similar to gb M87933 HUMAAALU364 Human carcinoma cell-derived Alu RNA transcript. (RNA); gb M86956 EPIDERMAL GROWTH FACTOR-LIKE CRIPTO PROTEIN (HUMAN); contains Alu repetitive element; contains MER4 repetitive element ;
5412	17959	30378	1.07	3.8E-01	H64927.1	EST_HUMAN	TRANSCRIPTION FACTOR SOX-10
5794	18419	31135	1.11	3.8E-01	Q04898	SWISSPROT	p10n protein [mink, Genomic, 2446 nt]
6481	19082		0.68	3.8E-01	S48925.1	NT	QV3-BT0537-271289-049-e02 BT0537 Homo sapiens cDNA
6737	19331	32137	5.29	3.8E-01	BE072398.1	EST_HUMAN	ta64f11.x1 Soares total Tetus Nb2HF8_gw Homo sapiens cDNA clone IMAGE:2047917 3' similar to contains Alu repetitive element;
6857	19591	32423	3.97	3.8E-01	AI374601.1	EST_HUMAN	

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7019	19517	32339	1.33	3.8E-01	AL161513.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 25
7525	20045		4.75	3.8E-01	X61597.1	NT	M. musculus gene for kallikrein-binding protein
8238	20779	33700	0.49	3.8E-01	M81385.1	NT	Mouse liver receptor homologous protein (LRH-1) mRNA, complete cds
8492	21031	33951	2.34	3.8E-01	AB046851.1	NT	Homo sapiens mRNA for KIAA1631 protein, partial cds
8560	21099	34019	1.14	3.8E-01	11441264	NT	Homo sapiens FOS-like antigen-1 (FOSL1), mRNA
8751	21290	34210	1.12	3.8E-01	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
9480	21679		4.03	3.8E-01	T95413.1	EST_HUMAN	y43h06.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:120539 5' similar to contains
11408	23859		3.5	3.8E-01	BE719219.1	EST_HUMAN	Alu repetitive element; contains PTR5 repetitive element.
11541	23989	37060	2.95	3.8E-01	R42550.1	EST_HUMAN	RCO-HT0841-040800-032-b12 HT0841 Homo sapiens cDNA
11541	23989	37061	2.95	3.8E-01	R42550.1	EST_HUMAN	y92h11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3'
11940	24272		2.81	3.8E-01	AE001124.1	NT	y92h11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3'
12059	24998		1.75	3.8E-01	U94788.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
12189	24421		1.45	3.8E-01	BE829256.1	EST_HUMAN	Human p53 (TP53) gene, complete cds
12565	24664		2.22	3.8E-01	U78031.1	NT	QV3-E10063-180700-271-405 E10063 Homo sapiens cDNA
12638	24713	30866	1.25	3.8E-01	AF194972.1	NT	Mus musculus apoptosis inhibitor bcl-x (bcl-x) gene, exon 3 and complete cds
2521	15085	27857	15.01	3.7E-01	AB037831.1	NT	Mus musculus developmental control protein mRNA, partial cds
3607	16112	28589	10.04	3.7E-01	AF056338.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3938	16536	29003	0.88	3.7E-01	AA319482.1	EST_HUMAN	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
4313	16899	29344	9.19	3.7E-01	AI218707.1	EST_HUMAN	EST21715 Adrenal gland tumor Homo sapiens cDNA 5' and
4412	16987	29440	1.18	3.7E-01	AW878037.1	EST_HUMAN	ak39c07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1510188 3'
4479	17064	29514	3.13	3.7E-01	AE002408.1	NT	MR3-OT0007-080300-104-b02 OT0007 Homo sapiens cDNA
5936	18557	31285	1.27	3.7E-01	AF135187.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 206 of the complete genome
6105	18721	31474	0.94	3.7E-01	AL163278.2	NT	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds
6633	19229	32033	1	3.7E-01	M10808.1	NT	Homo sapiens chromosome 21 segment HS21C078
6651	19247		0.81	3.7E-01	L10353.1	NT	Chicken (White leghorn) delta-1 and delta-2 crystallin genes, complete cds
7197	19728	32579	4.44	3.7E-01	11525843	NT	Mus satouda haploglobin mRNA, complete cds
8271	20812	33733	1.88	3.7E-01	11436739	NT	Homo sapiens tumor endofeital marker 7 precursor (TEM7), mRNA
8271	20812	33734	1.88	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8306	20847	33770	0.76	3.7E-01	AA02912.1	EST_HUMAN	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
9129	21664		1.54	3.7E-01	AJ271386.1	NT	ak43b11.s1 NC1 CGAP Le2 Homo sapiens cDNA clone IMAGE:1516701 3'
10074	22669		0.46	3.7E-01	K06991.1	NT	Gallus gallus mRNA for beta-carotene 15,15'-dioxygenase (bCOO gene)
10111	22608	35596	4.17	3.7E-01	AJ33941.1	EST_HUMAN	mouse Ig germline alpha membrane exons region
10809	23428	38446	3.47	3.7E-01	AJ287357.1	NT	qt46b07.x1 Soares fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950997 3'
							Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10909	23428	36447	3.47	3.7E-01	AJ287357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11341	23039	36048	4.81	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31)
11549	23997		1.6	3.7E-01	AA973540.1	EST_HUMAN	cd46d03.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1569221 3' similar to gb:M77698 TRANSCRIPTIONAL REPRESSOR PROTEIN YY1 (HUMAN);
11603	24046		2.76	3.7E-01	6677678	NT	Mus musculus retinoblastoma 1 (Rb1), mRNA
11640	24601		1.82	3.7E-01	J04982.1	NT	Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds
11821	24191		4.15	3.7E-01	AJ243525.1	NT	Chlamydomonas reinhardtii partial omp1 gene for outer membrane protein 1
11913	24251		4.72	3.7E-01	D66976.1	NT	Human mRNA for KIAA0223 gene, partial cds
12302	24499		2.94	3.7E-01	AL121154.1	EST_HUMAN	DKFZ762K075_r1 762 (synonym: hmd2) Homo sapiens cDNA clone DKFZp762K075 5'
12377	24545	30904	7.01	3.7E-01	Y18000.1	NT	Homo sapiens NF2 gene
282	12938	25424	1.07	3.6E-01	AJ009608.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
1033	13643		8.45	3.6E-01	U99241.1	NT	Human mbp gene, partial cds
1357	13951	26477	4.32	3.6E-01	T80255.1	EST_HUMAN	yd03e05.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24443 5'
1357	13951	26478	4.32	3.6E-01	T80255.1	EST_HUMAN	yd03e05.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24443 5'
1959	14543	27099	6.39	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2947419 3'
1959	14543	27100	6.39	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2947419 3'
1994	14576	27136	7.23	3.6E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2098	14677		0.88	3.6E-01	AF056927.1	NT	Rattus norvegicus repeat element associated with the Rasgrft1 gene
2309	14881		1.13	3.6E-01	AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2433	15000		2.49	3.6E-01	X76725.1	NT	P. irregularis (P3804) gene for actin
2528	15092	27665	3.34	3.6E-01	AW812033.1	EST_HUMAN	RC5-ST0171-181099-011-g07 ST0171 Homo sapiens cDNA
2659	15218	27789	1.38	3.6E-01	P24206	SWISSPROT	PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2824	18012		10.38	3.6E-01	AF199485.1	NT	Drosophila melanogaster sugar transporter 3 (sut3) mRNA, complete cds
3516	18121	28600	2.16	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
3516	18121	28601	2.16	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
4497	17081	29530	1.97	3.6E-01	BE707883.1	EST_HUMAN	RC1-HT0545-150600-014-b12 HT0545 Homo sapiens cDNA
4850	17428	29880	0.94	3.6E-01	AJ009608.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
4867	17443	29894	0.65	3.6E-01	Y11526.1	NT	Z. mays mRNA for casein kinase II alpha subunit
5153	17723	30154	2.28	3.6E-01	AW339093.1	EST_HUMAN	ha02g04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872566 3'
5261	17824	30249	0.58	3.6E-01	BE067698.1	EST_HUMAN	MR4-BT0358-270300-005-c10 BT0358 Homo sapiens cDNA
6236	18845	31616	1.16	3.6E-01	P16431	SWISSPROT	FORMATE HYDROGENLYASE SUBUNIT 5 PRECURSOR (FHL SUBUNIT 5) (HYDROGENASE-3 COMPONENT E)

Table 4

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6604	19201	32006	1.68	3.6E-01	Y10196.1	NT	Homo sapiens PHEX gene
7202	19733		4.57	3.6E-01	R04090.1	EST_HUMAN	y74a08.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:275987 5'
7327	19854	32717	1.73	3.6E-01	AW027174.1	EST_HUMAN	wf72c10.x1 Soares thymus_NHF Th Homo sapiens cDNA clone IMAGE:2513010 3' similar to TR.O15117
8166	20707	33623	0.68	3.6E-01	P98167	SWISSPROT	O15117 FYN BINDING PROTEIN. [1]:
8221	20762	33678	13.59	3.6E-01	AL161583.2	NT	SCO-SPONDIN
8632	21470	34386	3.06	3.6E-01	4504956	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
8632	21470	34386	3.06	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
8632	21470	34386	3.06	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
8932	21470	34386	3.06	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
9120	21656	34597	1.32	3.6E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9120	21834	34784	0.92	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9320	21834	34785	0.92	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9390	21813	34785	0.54	3.6E-01	X62825.1	NT	C.perringtonis plc gene for phospholipase C upstream region containing bent DNA fragment
9777	22275	35260	16.15	3.6E-01	Q63194	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN YATS
9904	22401	36374	0.53	3.6E-01	AW752801.1	EST_HUMAN	MR2-CT0222-211099-002-b10 CT0222 Homo sapiens cDNA
9604	22401	36375	0.53	3.6E-01	AW752801.1	EST_HUMAN	MR2-CT0222-211099-002-b10 CT0222 Homo sapiens cDNA
10823	23344	36359	2.51	3.6E-01	BE902390.1	EST_HUMAN	G0167641BF1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958997 5'
10827	23501	36531	4.15	3.6E-01	AB004293.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
11085	23577	36615	2.02	3.6E-01	L41687.1	NT	Mus musculus T-cell receptor V region delta 1 chain gene, 5' region
11318	23016	36025	4.07	3.6E-01	AE000856.1	NT	Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
11680	25109		2.45	3.6E-01	Y19210.1	NT	Homo sapiens HRB5 gene for hair keratin, exons 1 to 9
11768	24159		5.79	3.6E-01	AE000335.1	NT	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome
11923	24256		4.7	3.6E-01	U66888.1	NT	Mus musculus Emr1 mRNA, complete cds
12308	24502		2.16	3.6E-01		NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q23;q24)) translocated to, 10 (AF10). mRNA
120	12781	25273	1.35	3.5E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
223	12884	25369	2.67	3.5E-01	6678933	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
706	13327	25814	4.48	3.5E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
754	13373	25966	1.39	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
754	13373	25969	1.39	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
812	13430	26035	3.83	3.5E-01	BE126796.1	EST_HUMAN	S0181106R1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053961 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1682	14274	26807	1.91	3.5E-01	U35776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2322	14893	27469	1.12	3.5E-01	P06798	SWISSPROT	HOMEOBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3)
2637	15472	27770	1.92	3.5E-01	AA223252.1	EST_HUMAN	z08a09.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872 3'
2729	19284		11.8	3.5E-01	U05897.1	NT	Fibrobacter succinogenes S85 endoglucanase E (celE) and endoglucanase D (celD) gene, complete cds
3030	15646	28124	0.57	3.5E-01	AA057691.1	EST_HUMAN	28403.r1 Stratagene corneal stroma (#837222) Homo sapiens cDNA clone IMAGE:512285 5'
3878	16476		1.27	3.5E-01	AA642138.1	EST_HUMAN	nr60d03.s1 NCI_CGAP_Lym3 Homo sapiens cDNA clone IMAGE:1172357 3'
4349	16936	29377	2.3	3.5E-01	AF071253.1	NT	Danio rerio homeobox protein (hoxb5b) gene, complete cds
5014	17588	30031	0.57	3.5E-01	N81203.1	EST_HUMAN	788E1 fetal brain cDNA Homo sapiens cDNA clone 788E1-K similar to R07879, Z40498
5066	17639	30082	4.33	3.5E-01	M16349.1	NT	Rat leukocyte common antigen (L-Ca) gene, exons 1 through 5
5537	18169	30583	0.74	3.5E-01	Q96687	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5537	18169	30584	0.74	3.5E-01	Q96687	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5738	18364	31071	1.42	3.5E-01	D42045.1	NT	Human mRNA for KIAA0086 gene, complete cds
6384	18988		0.9	3.5E-01	AW863918.1	EST_HUMAN	PM4-SN0012-030400-001-a11 SN0012 Homo sapiens cDNA
6540	19139	31932	0.75	3.5E-01	AA431833.1	EST_HUMAN	zw70f03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782429 5' similar to TR:G1066635
6578	19176	31976	0.72	3.5E-01	U37150.1	NT	Bos taurus peptide methionine sulfoxide reductase (msrA) mRNA, complete cds
6770	19363	32172	0.93	3.5E-01	O24357	SWISSPROT	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHLOROPLAST PRECURSOR (G6PD)
7116	19456		3.51	3.5E-01	X86505.1	NT	S. scrofa mRNA for CD31 protein (PECAM-1)
8016	20558		2.02	3.5E-01	11448042	NT	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
8019	20561	33462	0.65	3.5E-01	BF558871.1	EST_HUMAN	RC4-ET0024-260600-014-d07 ET0024 Homo sapiens cDNA
8403	20943		0.61	3.5E-01	AF051561.1	NT	Rattus norvegicus Na-K-Cl cotransporter (Nkcc1) mRNA, complete cds
8857	21396	34319	1.12	3.5E-01	4507610	NT	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
9651	22160	35120	1.93	3.5E-01	Q02294	SWISSPROT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BIII)
9801	22299	35284	4.91	3.5E-01	Z6825.1	NT	Xlaevis gene for albumin including HP1 enhancer
9877	22374	35351	1.14	3.5E-01	BE174794.1	EST_HUMAN	QV2-HT0577-090400-128-c07 HT0577 Homo sapiens cDNA
10613	23146	38157	4	3.5E-01	X61084.1	NT	C.griseus rhodopsin gene for opsin protein
10902	23422	38440	2.09	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
10902	23422	38441	2.09	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11462	23912	38979	1.93	3.5E-01	N77697.1	EST_HUMAN	y280h12.r1 Soares_multiple sclerosis_2NBMSP Homo sapiens cDNA clone IMAGE:290375 5'
11532	23980	37050	1.71	3.5E-01	L05145.1	NT	Human glucokinase (GCK) gene, repeat polymorphism

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11778	25112		1.51	3.5E-01	AF297468.1	NT	Schistosoma mansoni strain NMRI chromatin assembly factor 1 small subunit-like protein (RBAP48) mRNA, complete cds
11851	24211		7.56	3.5E-01	X64565.1	NT	B.taurus atpA1 gene for F(0)F(1) ATP synthase alpha-subunit
12014	24313		2.03	3.5E-01	AE001774.1	NT	Thermotoga maritima section 86 of 136 of the complete genome
12209	24433		2.21	3.5E-01	AE001691.1	NT	Thermotoga maritima section 3 of 136 of the complete genome
12843	24950	30625	2.84	3.5E-01	H80814.1	EST_HUMAN	ys64f11.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
12843	24950	30626	2.84	3.5E-01	H80814.1	EST_HUMAN	ys64f11.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:219597 5'
738	13356		1.5	3.4E-01	AJ242956.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
1011	13621	26136	7.82	3.4E-01	Y09798.2	NT	Pseudomonas fluorescens colR, cds genes, orf222 and partial inaA gene
1013	13623	26138	8.97	3.4E-01	AW380120.1	EST_HUMAN	QV3-HT0261-241189-019-g10 HT0261 Homo sapiens cDNA
1371	13965	26491	1.86	3.4E-01	Y00554.1	NT	Azobacter vinelandii nifA gene for NifA protein (positive regulatory element)
2445	15012	27584	2.6	3.4E-01	D90909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3032	15648	28126	0.73	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3032	15648	28127	0.73	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3183	15796	28268	0.96	3.4E-01	D90909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3197	15809	28262	6.76	3.4E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGB1) mRNA, complete cds
3387	15996	28473	0.84	3.4E-01	AF034862.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3584	16188	28671	4.84	3.4E-01	AF106835.1	NT	Methylovorus sp. strain SS1 putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3858	16456		1.32	3.4E-01	BF449010.1	EST_HUMAN	Tn84a01.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q9UJ15
4108	16702		1.23	3.4E-01	AF184614.1	NT	Q9UJ15 DJ18C9.1
4126	16718		1.56	3.4E-01	AA584196.1	EST_HUMAN	Homo sapiens p47-phox (NCF1) gene, complete cds
4594	17177	28624	0.7	3.4E-01	AF166341.1	NT	no11b10.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'
4749	17330	28773	2	3.4E-01	BE069912.1	EST_HUMAN	Homo sapiens integrin alpha 6 (ITGA6) gene, exons 12 through 23
4765	17346	29795	1.01	3.4E-01	BF314689.1	EST_HUMAN	MIR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA
5087	17660		4.2	3.4E-01	AI240973.1	EST_HUMAN	601901632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130935 5'
5864	18486	31210	2.9	3.4E-01	AL161594.2	NT	q95c05.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains Alu repetitive element
5978	18599		5.68	3.4E-01	AA085313.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
6158	18771		2.44	3.4E-01	L02971.1	NT	zn12a11.s1 Stralagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:547221 3'
							Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6181	18791	31560	0.69	3.4E-01	BE748912.1	EST_HUMAN	801571811T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838826 3'
6256	18865	31635	2.45	3.4E-01	AW204505.1	EST_HUMAN	U1-HB11-ae-e-12-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2719582 3'
6382	18886	31768	1.62	3.4E-01	AL120544.1	EST_HUMAN	DKFZp761A249_1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A249 5'
6841	19431		1.32	3.4E-01	N95225.1	EST_HUMAN	zb53a12.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:307342 3'
7027	19561	32388	1.09	3.4E-01	AI468082.1	EST_HUMAN	Im63g05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:S37431 LAMININ RECEPTOR (HUMAN).
7847	20389		0.51	3.4E-01	AE000493.1	NT	Escherichia coli K-12 MG1655 section 383 of 400 of the complete genome
8179	20720	33635	0.51	3.4E-01	Y14930.1	NT	Homo sapiens TCRV28 gene, allele A4, partial
8424	20984		1.92	3.4E-01	AA337063.1	EST_HUMAN	EST41765 Endometrial tumor Homo sapiens cDNA 5' end
8498	21037	33958	0.88	3.4E-01	L04690.1	NT	Cricetus griseus cholesterol 7-alpha-hydroxylase gene, complete cds
8786	21325	34249	1.63	3.4E-01	9633624	NT	Bovine enterovirus strain K2577, complete genome
9139	21674	34617	3.89	3.4E-01	P26013	SWISSPROT	INTEGRIN BETA-3 PRECURSOR
9342	21856		3.89	3.4E-01	P26013	SWISSPROT	INTEGRIN BETA-3 PRECURSOR
9367	20306	33208	4.77	3.4E-01	AB017510.1	NT	Ephydra fluviatilis mRNA for PLC-gammaS, complete cds
9367	20306	33209	4.77	3.4E-01	U19492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9612	22112	35075	0.88	3.4E-01	U68763.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9804	22302	35288	1.99	3.4E-01	AJ225084.1	NT	Glycine max putative transcription factor SCOF-1 (scof-1) mRNA, complete cds
10373	22887		0.54	3.4E-01	AE004096.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18
10895	23416		4.42	3.4E-01	AE000881.1	NT	Vibrio cholerae chromosome I, section 4 of 251 of the complete chromosome
10932	23450	36471	2.61	3.4E-01	P06925	SWISSPROT	Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (section 87 of 148) of the complete genome PROBABLE E4 PROTEIN.
10969	23484	36512	2.72	3.4E-01	AF045981.1	NT	Rutillus arcasii cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11164	23671	36716	1.89	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
11164	23671	36717	1.89	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
11372	23824	36887	2.27	3.4E-01	AB035507.1	NT	Rattus norvegicus mRNA for s-glycerin/MUC18, complete cds
11401	23852	36917	4.36	3.4E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
11614	24056	37121	1.75	3.4E-01	BF081948.1	EST_HUMAN	7k69d12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3480846 3'
11655	24082		2.12	3.4E-01	U93604.1	NT	Citrus variegation virus putative replicase gene, partial cds
11771	24160		1.44	3.4E-01	Z21621.1	NT	S. cerevisiae RIB5 gene encoding Riboflavin synthase
11873	24836		1.8	3.4E-01	AF254351.1	NT	Schizosaccharomyces pombe Cwifp (cwif) gene, complete cds
11986	24303		14.59	3.4E-01	L26339.1	NT	Human autoantigen mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12023	24865		3.18	3.4E-01	BE218652.1	EST_HUMAN	h42h08.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.i3
12079	24874		2.44	3.4E-01	9838381	NT	PTR5 repetitive element;
12196	24424	30950	2.66	3.4E-01	AJ287131.1	NT	Beta vulgaris mitochondrion, complete genome
12427	25068		1.25	3.4E-01	AJ288948.1	NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
							Clostridium cellulidicum partial spoIVB gene and spoIA gene, strain ATCC 35319
12523	24839		2.55	3.4E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes, >
12651	24723		2.71	3.4E-01	11468174	NT	Naegleria gruberi mitochondrion, complete genome
16	12895	25151	13.68	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
110	12895	25151	3.75	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
473	13108	25599	1.08	3.3E-01	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
661	13285	25766	1.97	3.3E-01	7662485	NT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
1242	13840	26358	2.96	3.3E-01	Q12448	SWISSPROT	PROLINE-RICH PROTEIN LAS17
1350	13945	26469	3.58	3.3E-01	BF568880.1	EST_HUMAN	6021840161 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3'
1649	14241	26775	1.43	3.3E-01	8753685	NT	Mus musculus disintegrin 5 (Dign5), mRNA
1773	14363		1.44	3.3E-01	AA332734.1	EST_HUMAN	EST38722 Embryo, 8 week I Homo sapiens cDNA 5' end
2075	14655		1.22	3.3E-01	AF031148.1	NT	Methylococcus capsulatus strain Bath outer membrane protein MopB (mopB) gene, complete cds
2450	15017		5.41	3.3E-01	4507834	NT	Homo sapiens uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS) mRNA
2978	15592	28074	2.14	3.3E-01	AJ251805.1	NT	Bacteriophage phi-Ye03-12 complete genome
3049	15865		0.86	3.3E-01	O02743	SWISSPROT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P35)
3091	15708	28178	0.82	3.3E-01	AJ007932.2	NT	Streptomyces argillaceus mithramycin biosynthetic genes
3542	16147	28629	0.99	3.3E-01	AB012922.1	NT	Homo sapiens MTA1-L1 gene, complete cds
3862	16480	28942	2.14	3.3E-01	O84645	SWISSPROT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3890	16489	28949	0.85	3.3E-01	P22602	SWISSPROT	GENOME POLYPROTEIN[CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3]
4037	16635	29104	1.49	3.3E-01	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4073	16669	29130	1.95	3.3E-01	AF200446.1	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4457	17043		1.44	3.3E-01	D31682.1	NT	Rattus norvegicus DNA for regucalcin, partial cds
4799	17377		1.57	3.3E-01	AI539114.1	EST_HUMAN	tp78b12.x1 NCI CGAP_U13 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gb:X57522 ANTIGEN PEPTIDE TRANSPORTER 1 (HUMAN);
4964	17538	29980	1.44	3.3E-01	D56403.1	NT	Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2868766

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5527	18159	30573	2.75	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
5527	18159	30574	2.75	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
6101	18717	31468	1.72	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6101	18717	31469	1.72	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6188	18798	31567	12.71	3.3E-01	P05691	SWISSPROT	CIRCUJMSPOROZOITE PROTEIN (CS)
6969	19546	32369	4.8	3.3E-01	AI628131.1	EST_HUMAN	ty84h01.x1 NCL_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
6969	19546	32370	4.8	3.3E-01	AI628131.1	EST_HUMAN	ty84h01.x1 NCL_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
7758	20266	33162	1.61	3.3E-01	N85146.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT
8497	21036	33957	17.55	3.3E-01	BF683954.1	EST_HUMAN	602140372F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301800 5'
8663	21202	34120	0.48	3.3E-01	BF210322.1	EST_HUMAN	601873281F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097180 5'
8696	21235	34157	0.49	3.3E-01	AU126115.1	EST_HUMAN	AU126115 Homo sapiens cDNA clone NT2RP1000130 5'
8696	21235	34158	0.49	3.3E-01	AU126115.1	EST_HUMAN	AU126115 NT2RP1 Homo sapiens cDNA clone NT2RP1000130 5'
9042	21579	34508	0.83	3.3E-01	Q62925	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (MAPK/ERK KINASE 1) (MEK1)
9300	21900	34848	0.99	3.3E-01	BE828461.1	EST_HUMAN	CM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
9300	21900	34849	0.99	3.3E-01	BE828461.1	EST_HUMAN	CM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
9430	21939	34887	3.24	3.3E-01	N68966.1	EST_HUMAN	za67h01.s1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:297649 3'
9471	21870	34819	2.93	3.3E-01	BF376745.1	EST_HUMAN	RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
9902	22399		2.16	3.3E-01	L41044.1	NT	Homo sapiens high-mobility group phosphoprotein (HMGI-C) gene, exons 1-3, complete cds
10600	23134	36147	2.93	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
10600	23134	36148	2.93	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
10905	23424		1.8	3.3E-01	BF526499.1	EST_HUMAN	602070802F1 NCL_CGAP_Brr84 Homo sapiens cDNA clone IMAGE:4213585 5'
11110	23620	36661	17.52	3.3E-01	BE219351.1	EST_HUMAN	tv61g02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3'
11223	23754	36812	4.97	3.3E-01	P47953	SWISSPROT	GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (ICE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-28) (CBP30)
11565	24012		4.68	3.3E-01	AA08621.1	EST_HUMAN	cb71g02.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336850 3'
11584	12695	25151	2.48	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5J nodX gene
11759	24153	36771	1.96	3.3E-01	6598319	NT	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA
12510	24631		36.28	3.3E-01	AF000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt, position (2/7)
482	13115		1.79	3.2E-01	AF018261.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
747	13367		0.76	3.2E-01	AL161561.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1204	13804	26317	27.96	3.2E-01	AF047013.1	NT	Fusarium rose virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1325	13919	28441	1.39	3.2E-01	Z50202.1	NT	P. vulgaris arc5-1 gene
1434	14027	26555	7.37	3.2E-01	Q48624	SW/SSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1811	14401	26848	0.92	3.2E-01	Z36041.1	NT	S. cerevisiae chromosome II reading frame ORF YBR172c
1819	14409	26954	6.36	3.2E-01	AW957194.1	EST_HUMAN	EST369264 MAGe resequences; MAGD Homo sapiens cDNA
1819	14409	26955	6.36	3.2E-01	AW957194.1	EST_HUMAN	EST369264 MAGe resequences; MAGD Homo sapiens cDNA
1883	14469	27026	1.22	3.2E-01	AL111655.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2205	14781	27354	2.89	3.2E-01	BF203817.1	EST_HUMAN	601868904F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5'
2578	15140		2.24	3.2E-01	7710079	NT	Mus musculus Pbx/knotted 1 homeobox (Pbxox1), mRNA
2734	15289	27857	1.09	3.2E-01	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
3668	16269		0.78	3.2E-01	D10872.1	NT	Human h NAT allele 3-2 gene for arylamine N-acetyltransferase
4023	16621		0.61	3.2E-01	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
4483	17068	29518	1.64	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4597	17181	29628	1.56	3.2E-01	Q10268	SW/SSPROT	HYPOTHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME 1 PRECURSOR
4844	17422		6.52	3.2E-01	BF693617.1	EST_HUMAN	602081972F1 NIH_MGC_31 Homo sapiens cDNA clone IMAGE:4246505 5'
5009	17582	30025	0.63	3.2E-01	Q57081	SW/SSPROT	CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 3 (CYTADHERENCE ACCESSORY PROTEIN 3) (ACCESSORY ADHESIN PROTEIN 3) (P69)
5174	17741	30170	0.58	3.2E-01	BE782748.1	EST_HUMAN	601465591F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3868799 5'
5382	17850	30363	0.93	3.2E-01	AY008847.1	NT	Homo sapiens interleukin 12 p40 subunit (IL12B) gene, IL12B-1 allele, complete cds
5476	18110	30519	2.5	3.2E-01	BE173964.1	EST_HUMAN	CMO-HT0568-060300-268-f10 HT0568 Homo sapiens cDNA
6112	18128	31481	1.18	3.2E-01	L27221.1	NT	Giardia intestinalis pyruvate:flavodoxin oxidoreductase and flanking genes
6831	19421		1.03	3.2E-01	AB002359.1	NT	Human mRNA for KIAA0361 gene, KIAA0361 protein
8113	20654	33563	1.33	3.2E-01	M60266.1	NT	Rat ISO-atrial natriuretic factor gene, complete cds
8210	20751	33865	0.51	3.2E-01	AJ231001.1	NT	Rattus norvegicus repeat, map NOS-D12Wox1
8308	20849	33772	11.34	3.2E-01	X02508.1	NT	H. sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
8311	20852	33777	16.78	3.2E-01	BF311635.1	EST_HUMAN	601867107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126633 5'
8398	20838		1.43	3.2E-01	AL161574.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70
8437	20877	33891	1.22	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:4075627 5'
8437	20877	33892	1.22	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:4075627 5'
8508	21047	33968	2.72	3.2E-01	AE02015.1	NT	Deinococcus radiodurans R1 section 152 of 229 of the complete chromosome 1
8605	21144	34058	0.69	3.2E-01	U51020.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V region (VH6-a2) gene, partial cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8605	21144	34059	0.69	3.2E-01	U51026.1	NT	Oryzotagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds
8997	21535	34465	0.58	3.2E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9007	21544		2.08	3.2E-01	M86511.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
9077	21613	34547	0.48	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9077	21613	34548	0.48	3.2E-01	AF041829.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9905	22402	35376	3.22	3.2E-01	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes
10100	22595	35586	0.51	3.2E-01	BE326230.1	EST_HUMAN	h9905.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181568 3'
10213	22708		3.03	3.2E-01	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
10548	23084	36098	3.28	3.2E-01	T06813.1	EST_HUMAN	EST04702 Fetal brain, Stralagene (cat#936206) Homo sapiens cDNA clone HF8DZ21
11786	24969		4.31	3.2E-01	L07288.1	NT	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds
12344	24525		4.65	3.2E-01	D83217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
12441	24819		3.37	3.2E-01	AF157825.1	NT	Bos taurus insulin 1,4,5-bisphosphate receptor type I mRNA, complete cds
12489	24618		1.94	3.2E-01	L39874.1	NT	Homo sapiens deoxycytidylate deaminase gene, complete cds
12550	25041	30504	1.98	3.2E-01	BE385776.1	EST_HUMAN	601275480F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616746 5'
2695	15252	27823	2.39	3.1E-01	R18051.1	EST_HUMAN	ye90H08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to
2722	15403	27843	3.67	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2722	15403	27844	3.67	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2883	15501		1.35	3.1E-01	AW629036.1	EST_HUMAN	h46H08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2875391 3'
3208	15620		3.53	3.1E-01	AB029089.1	NT	Mus musculus gene for Ser/Thr Kinase KKIAMRE, exon 6
3978	16576	29046	0.91	3.1E-01	AJ251586.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
5055	17628	30072	0.79	3.1E-01	S68245.1	NT	carbonic anhydrase IV [rats, Sprengel-Dawley, lung, mRNA, 1205 nt]
5097	17670	30109	0.82	3.1E-01	AE003984.1	NT	Xylella fastidiosa, section 130 of 229 of the complete genome
5206	17771	30194	0.98	3.1E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
5669	18296	30776	10.8	3.1E-01	AF176111.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5786	18411	31127	0.75	3.1E-01	Z74883.1	NT	S.cerevisiae chromosome XV reading frame ORF YOL141w
5796	18421		0.99	3.1E-01	Y13278.1	NT	Mus musculus mRNA for polycystin
5945	18565	31295	2.16	3.1E-01	AF184122.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22
6592	19189	31992	2.63	3.1E-01	AW983549.1	EST_HUMAN	RC3-HN0001-310300-011-b04 HN0001 Homo sapiens cDNA
6654	19250	32052	0.87	3.1E-01	AI264458.1	EST_HUMAN	q139d01.x1 NCI_CGAP_Co6 Homo sapiens cDNA clone IMAGE:1874689 3'
6784	19375	32191	0.81	3.1E-01	X71887.1	NT	H.sapiens gene for immunoglobulin kappa light chain variable region A8 and A9
6863	19597		0.9	3.1E-01	AW377354.1	EST_HUMAN	MR2-C10222-281099-005-h05 C10222 Homo sapiens cDNA

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7048	24741	30458	2.4	3.1E-01	BE737392.1	EST_HUMAN	601306121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640420 5'
7871	20183	33071	1.18	3.1E-01	4885390	NT	Homo sapiens hyaluronan synthase 2 (HAS2), mRNA
8582	21121	34041	1.22	3.1E-01	R45318.1	EST_HUMAN	Yd48701.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35639 3'
8816	22314	35285	0.45	3.1E-01	6676322	NT	Mus musculus phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma (Pip5k1c), mRNA
9979	22474	35456	0.81	3.1E-01	BF686839.1	EST_HUMAN	602124743F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4281611 5'
9978	22474	35457	0.81	3.1E-01	BF686839.1	EST_HUMAN	602124743F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4281611 5'
10035	22530	35525	1.7	3.1E-01	A1244001.1	EST_HUMAN	q161e11.x1 NCLCGAP_Kid3 Homo sapiens cDNA clone IMAGE:1863990 3' similar to gb:355700 HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAN);
10204	22699		0.54	3.1E-01	T55325.1	EST_HUMAN	Yb47n08.s1 Striatogene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:74387 3' similar to similar to gb:M91036_maz2 HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS (HUMAN)
10717	23245	38261	1.95	3.1E-01	BF216117.1	EST_HUMAN	601883592F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095814 5'
11411	23862	36923	2.03	3.1E-01	7662291	NT	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA Andis opalinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
11921	24257		2.13	3.1E-01	AF294308.1	NT	Sitostation vitreum 40S ribosomal protein S11 mRNA, partial cds
11960	24282		1.95	3.1E-01	AF304192.1	NT	Homo sapiens membrane-bound aminopeptidase P (NPEP2) gene, complete cds
12108	24370		3.31	3.1E-01	AF189893.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, complete cds; and L-type calcium channel $\alpha 2$
12496	24824		3.89	3.1E-01	AF196779.1	NT	JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaplophysin genes, complete cds
12535	25035		1.82	3.1E-01	10946623	NT	Mus musculus peptidoglycan recognition protein-like (Pglyrp1-pending), mRNA
76	15382	25234	1.37	3.0E-01	6755083	NT	Mus musculus protein kinase C, epsilon (Pkc), mRNA
275	12832	25419	11.51	3.0E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
1266	13663	26380	2.05	3.0E-01	AW300400.1	EST_HUMAN	xs63f08.x1 NCLCGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
1555	14147	26680	6.64	3.0E-01	AJ006755.1	NT	Baleenoptera physalus gene encoding atrial natriuretic peptide
3248	15860		1.4	3.0E-01	AB030481.1	NT	Corynebacterium sp. ALY-1 alrPG gene for polyglutamate lyase, complete cds
3632	16530	28997	2.1	3.0E-01	AW817785.1	EST_HUMAN	PM1-ST0262-261199-001-g01 ST0262 Homo sapiens cDNA
4046	16643	29109	1.01	3.0E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
4811	17194	29640	1.78	3.0E-01	AJ006755.1	NT	Baleenoptera physalus gene encoding atrial natriuretic peptide
5554	18186	30601	5.34	3.0E-01	BE741629.1	EST_HUMAN	60158460F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5'
5627	18256	30726	0.88	3.0E-01	AF229247.1	NT	Canlagalo orthopoxvirus hemagglutinin gene, complete cds
5695	18321	30820	4.03	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5695	18321	30821	4.03	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-a03 BT0333 Homo sapiens cDNA
5731	18357	31082	4.57	3.0E-01	U01247.1	NT	Mus musculus 129/sv Clara cell 10 kd protein (mCC10) gene, complete cds
6919	18678	32407	3.14	3.0E-01	D16313.1	NT	Mouse cytokeratin 15 gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6844	18052	30475	0.7	3.0E-01	U02369.1	NT	Strongylocentrotus purpuratus 34/67 kDa laminin-binding protein mRNA, partial cds
7005	19503	32322	0.96	3.0E-01	AF229247.1	NT	Cantagalo orthopoxvirus hemagglutinin gene, complete cds
7175	19707	32555	0.76	3.0E-01	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
7367	18893	32758	6	3.0E-01	10947007	NT	Mus musculus midnolin (Midn-pending), mRNA
7512	20033	32899	1.88	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBL5 PspA (pspA) gene, partial cds
7887	20409	33316	1.07	3.0E-01	AE001755.1	NT	Thermotoga maritima section 67 of 136 of the complete genome
8314	20855		3.82	3.0E-01	9910161	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clectsf9), mRNA
8411	20951	33870	1.27	3.0E-01	BE568083.1	EST_HUMAN	601339079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3881594 5'
8763	21302	34223	0.82	3.0E-01	AF141676.1	NT	Streptomyces sulfonolactams isopenicillin N synthase (pcbC) gene, partial cds
8805	21344		0.95	3.0E-01	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
9145	21680	34924	0.98	3.0E-01	AF220507.1	NT	Anabaena POC7120 cytosine-specific DNA methyltransferase (dnmB) gene, complete cds; putative anthranilate phosphoribosyltransferase gene, partial cds; and unknown gene
9403	21993	34949	0.56	3.0E-01	P76389	SWISSPROT	HYPOTHETICAL 59.5 KD PROTEIN IN WZA-ASMA INTERGENIC REGION
9878	22375	35352	0.84	3.0E-01	BF574612.1	EST_HUMAN	602133271F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288336 5'
10294	22788	35778	0.56	3.0E-01	AW118111.1	EST_HUMAN	xe03d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2806035 3'
10296	22780	35780	1.95	3.0E-01	AB030231.1	NT	Aspergillus oryzae bipA gene for ER chaperone BiP, complete cds
10315	22809	35801	0.73	3.0E-01	BF683841.1	EST_HUMAN	602140133F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301097 5'
10315	22809	35802	0.73	3.0E-01	BF683841.1	EST_HUMAN	602140133F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4301097 5'
11604	24047	37112	2.87	3.0E-01	H51028.1	EST_HUMAN	yp84p10.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:194107 5'
11604	24047	37113	2.87	3.0E-01	H51028.1	EST_HUMAN	yp84p10.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:194107 5'
11975	24287		1.37	3.0E-01	P54680	SWISSPROT	PONTICULIN PRECURSOR
12227	24984		2.93	3.0E-01	AJ297631.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
12529	25033		2.51	3.0E-01	6677768	NT	Mus musculus ribose 5-phosphate isomerase A (Rpia), mRNA
1924	14509	27064	2.27	2.9E-01	5174502	NT	Homo sapiens membrane component, chromosome 11, surface marker 1 (M11S1) mRNA
2070	14650	27221	1.38	2.9E-01	AE000736.1	NT	Aquifex aeolicus section 68 of 109 of the complete genome
2524	15088		1.22	2.9E-01	M32360.1	NT	Mouse apolipoprotein A-II (AIIp-2) gene, complete cds
3289	15900	28379	2.07	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171299-001-f12 CT0326 Homo sapiens cDNA
3289	15900	28380	2.07	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171299-001-f12 CT0326 Homo sapiens cDNA
3665	16563	29032	0.71	2.9E-01	A1610836.1	EST_HUMAN	tp21a11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gb:D15050 NIL-2-A
4159	16751		0.67	2.9E-01	AW002802.1	EST_HUMAN	ZINC FINGER PROTEIN (HUMAN); contains element L1 repetitive element ;
							wf02f10.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2480395 3'
4583	17166	29609	1.21	2.9E-01	AA284468.1	EST_HUMAN	zs57d12.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Alu repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4763	17372		0.63	2.9E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
5148	17718		1.02	2.9E-01	U90756.1	NT	Lymnaea dispar vitellogenin gene, complete cds
5154	17724	30155	1.43	2.9E-01	7862169	NT	Homo sapiens KIAA0537 gene product (KIAA0537), mRNA
5285	17847		1.7	2.9E-01	AI670899.1	EST_HUMAN	w60603.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297309 3' similar to contains L1.12 L1 repetitive element;
5483	18098		1.25	2.9E-01	R37485.1	EST_HUMAN	y77e12.s1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:28291 3'
5592	19522	32344	0.79	2.9E-01	AF321001.1	NT	Suaeda maritima subsp. salsa S-adenosylmethionine synthetase 2 mRNA, complete cds
5937	18558	31286	5.1	2.9E-01	X58098.1	NT	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase
5937	18558	31287	5.1	2.9E-01	X58098.1	NT	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase
5948	18570	31302	6.06	2.9E-01	6678662	NT	system polypeptides P16, 18, 28, 30 and levanase
6206	18816	31597	1.26	2.9E-01	AA418145.1	EST_HUMAN	Mus musculus Eph receptor A8 (EphA8), mRNA
6427	19030	31813	0.93	2.9E-01	AI797128.1	EST_HUMAN	z97b12.r1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:767711 5'
6467	19088	31854	2.3	2.9E-01	U03420.1	NT	repetitive element;
6585	19183	31983	0.72	2.9E-01	R69184.1	EST_HUMAN	Bos taurus myosin I mRNA, complete cds
6585	19183	31984	0.72	2.9E-01	R69184.1	EST_HUMAN	y39d08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5'
7082	18081	30437	1.35	2.9E-01	AF142329.1	NT	y39d08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5'
7153	19885	32527	2.87	2.9E-01	Q04399	SWISSPROT	Mus musculus Filin protein (Filin) gene, complete cds; and Ligh protein (Ligh) gene, partial cds PUTATIVE MULTICOPPER OXIDASE YDR509C
7213	19744	32598	1.61	2.9E-01	AF100956.1	NT	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1, 3-galactosyl tr>
7860	20402	33308	1.92	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
7860	20402	33309	1.92	2.9E-01	BE540422.1	EST_HUMAN	601065830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8103	20844		0.89	2.9E-01	BF217743.1	EST_HUMAN	601882570F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095113 5'
8531	21070	33990	0.66	2.9E-01	AJ150910.1	EST_HUMAN	AU150910 NT2RP2 Homo sapiens cDNA clone NT2P2003901 3'
8856	21385	34318	1.07	2.9E-01	AF225908.1	NT	Arabidopsis thaliana sulfonylurea receptor-like protein mRNA, complete cds
8963	21501	34423	0.71	2.9E-01	M22452.1	NT	Baboon lymphocyte homing/adhesion receptor mRNA, complete cds
9170	21747	34688	0.77	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
9170	21747	34689	0.77	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
10773	23267	36302	2.24	2.9E-01	AF128843.1	NT	Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
11041	23555	36598	2.88	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11041	23555	36590	2.88	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11453	23903	36970	2.07	2.9E-01	AA835373.1	EST_HUMAN	ny35h02.s1 NCL_CGAP_Prl2 Homo sapiens cDNA clone IMAGE:1273779 similar to contains LTR8.12 LTR8
11458	23906	36973	5.52	2.9E-01	AL139078.2	NT	repetitive element ;
12172	24411	30944	1.54	2.9E-01	AW005671.1	EST_HUMAN	w28805.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2565921 3' similar to contains element
12262	24472	30932	1.47	2.9E-01	AF092453.1	NT	repetitive element ;
12313	24505		1.4	2.9E-01	BE788189.1	EST_HUMAN	Hom sapiens TNF-a-inducible RNA binding protein (TIRP) gene, complete cds
12586	24679	30877	1.57	2.9E-01	Y06937.1	NT	601482059F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884559 5'
12586	24679	30878	1.57	2.9E-01	Y06937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
594	13224		2.06	2.8E-01	U67136.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
599	13228		0.75	2.8E-01	L28145.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
1122	13725	26238	3.14	2.8E-01	AF168050.1	NT	Prune dwarf virus movement protein, complete cds; coat protein, complete cds
1320	13914	26435	3.51	2.8E-01	BE313442.1	EST_HUMAN	Guira guira oocyte maturation factor Mos (c-mos) gene, partial cds
1320	13914	26436	3.51	2.8E-01	BE313442.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1334	13928	26448	1.03	2.8E-01	D96550.1	NT	Human mRNA for serine/threonine protein kinase, complete cds
1765	14355	26902	2.01	2.8E-01	AW86020.1	EST_HUMAN	QV1-CT0364-120200-085-b05 CT0364 Homo sapiens cDNA
2057	14638	27210	2.12	2.8E-01	AL047620.1	EST_HUMAN	DKFZp586i2321_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586i2321
2175	14752	27322	3.53	2.8E-01	AW511195.1	EST_HUMAN	hd44b03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912333 3'
2511	15075	27648	2.41	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2511	15075	27649	2.41	2.8E-01	AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2584	15147		2.75	2.8E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2688	15246	27813	1.21	2.8E-01	AB020975.1	NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds
2988	15614		1.7	2.8E-01	AF179480.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
2989	15615	28094	2.36	2.8E-01	Z14037.1	NT	B.taurus microsatellite (ETH121)
2989	15615	28095	2.36	2.8E-01	Z14037.1	NT	B.taurus microsatellite (ETH121)
3425	16033	28513	1.26	2.8E-01	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt, position (4/7)
4068	16664	29125	2.06	2.8E-01	AE001180.1	NT	Borrelia burgdorferi (section 66 of 70) of the complete genome
4202	16791		0.62	2.8E-01	AE004450.1	NT	Pseudomonas aeruginosa PA01, section 11 of 528 of the complete genome
4276	16862		2.75	2.8E-01	A090868.1	EST_HUMAN	ov44g10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640226 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;
4553	17136	29584	1.32	2.8E-01	AL021127.2	NT	Mus musculus chromosome X contigA, putative Magea9 gene, Caltractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
4558	17142	29590	2.47	2.8E-01	P13615	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4897	17472	29828	1.07	2.8E-01	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4897	17472	28929	1.07	2.8E-01	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4937	17512	28958	1.02	2.8E-01	AW594539.1	EST_HUMAN	hg68405.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:2850568 3'
4949	17524	28965	1.17	2.8E-01	AF075238.1	NT	Hepatitis G virus isolate 60 (SZNAE12) polyprotein precursor, gene, partial cds
4955	17530	28972	3.5	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4986	17560	30003	1.87	2.8E-01	BF528188.1	EST_HUMAN	602042601F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4180129 5'
5013	17587	30030	2.82	2.8E-01	A1272689.1	EST_HUMAN	q159c11.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu repetitive element; contains element LTR5 repetitive element;
5514	24744	30558	21.59	2.8E-01	AA349987.1	EST_HUMAN	EST57072 Infant brain Homo sapiens cDNA 5' end
5791	18416	31132	2.76	2.8E-01	AB016625.1	NT	Homo sapiens OCTN2 gene, complete cds
5983	18603		0.97	2.8E-01	AW992583.1	EST_HUMAN	GM1-BIN0024-150200-118-g12 BN0024 Homo sapiens cDNA
6078	18695	31442	0.69	2.8E-01	AA765296.1	EST_HUMAN	oa01d06.s1 NCI_CGAP_Co81 Homo sapiens cDNA clone IMAGE:1303691 3' similar to gb:M34539 FK506-BINDING PROTEIN (HUMAN);
6323	25114		0.75	2.8E-01	M36668.1	NT	Bovine 880 bp repeated unit of 1.723 satellite DNA
6366	18970	31748	1.55	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-biphosphate aldolase mRNA, complete cds
6366	18970	31749	1.55	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-biphosphate aldolase mRNA, complete cds
6828	19419	32235	8.4	2.8E-01	BF511215.1	EST_HUMAN	U1-H-B14-act-f04-0-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3'
7487	19989		1.19	2.8E-01	U05633.1	NT	Marsilea quadrifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcL) gene, chloroplast gene encoding chloroplast protein, partial cds
7768	20276	33174	0.69	2.8E-01	BE537151.1	EST_HUMAN	607063105F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449569 5'
8038	20578	33482	1.12	2.8E-01	A1346126.1	EST_HUMAN	qp48h01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1
8038	20578	33483	1.12	2.8E-01	A1346126.1	EST_HUMAN	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8150	20691	33605	2.16	2.8E-01	U51688.1	NT	qp48h01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1
8451	20991	33909	0.47	2.8E-01	AA911628.1	EST_HUMAN	Homo sapiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5
8525	21064		6.69	2.8E-01	BF347847.1	EST_HUMAN	q02h05.s1 NCI_CGAP_Co12 Homo sapiens cDNA clone IMAGE:1419993 3' similar to gb:M87789 IG
9387	21810	34761	1.22	2.8E-01	U17251.1	NT	GAMMA-1 CHAIN C REGION (HUMAN);
9627	22127		1.03	2.8E-01	L13654.1	NT	602022987F1 NCI_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4158525 5'
9803	22301	35286	1.04	2.8E-01	AF132728.1	NT	Neurospora crassa negative regulator sulfur controller-2 (scc-2) gene, complete cds
9803	22301	35287	1.04	2.8E-01	AF132728.1	NT	Lycopodium obscurum peroxidase (TPX1) mRNA, complete cds
9803	22301	35287	1.04	2.8E-01	AF132728.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
9861	22358	35338	0.64	2.8E-01	AF294393.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
9972	22467	35451	1.91	2.8E-01	7706163	NT	Rattus norvegicus glycerol-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b; nuclear gene for mitochondrial product
							Homo sapiens hypothetical protein (LOC51319), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10215	22710		0.81	2.8E-01	8626154	NT	Fujinami sarcoma virus, complete genome
10255	22750	35738	0.47	2.8E-01	BE959727.2	EST_HUMAN	60165482R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839765 3'
10622	23154	36166	2.26	2.8E-01	BF241062.1	EST_HUMAN	601850794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
10622	23154	36167	2.26	2.8E-01	BF241062.1	EST_HUMAN	601850794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
10651	23183	36197	2.83	2.8E-01	BF695970.1	EST_HUMAN	601852148F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076026 5'
10780	23284	36297	3.31	2.8E-01	AF051882.1	NT	Drosophila heteroneura fruitless (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds
11158	23655		4.56	2.8E-01	BF674023.1	EST_HUMAN	60213741BF1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273853 5'
12213	24436		15.74	2.8E-01	D83329.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
12328	24514	30920	8.89	2.8E-01	BE178699.1	EST_HUMAN	PM4-HT0606-030400-001-407 HT0606 Homo sapiens cDNA
12356	24533	30927	1.25	2.8E-01	BE900116.1	EST_HUMAN	601873020F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955996 5'
12519	24868		2.21	2.8E-01	11433629	NT	Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA
502	13134	25622	3.21	2.7E-01	Y17324.1	NT	Rattus norvegicus CDK104 mRNA
641	13264	25740	2.53	2.7E-01	AA450091.1	EST_HUMAN	z39h10.s1 Soares_tet1_fetus_Nb2HFB_9w Homo sapiens cDNA clone IMAGE:788827 3' similar to contains Alu repetitive element
1304	13898	26418	1.69	2.7E-01	AB004906.1	NT	Ipomoea purpurea transposable element Tip100 gene for transposase, complete cds
1662	14255		2.17	2.7E-01	X79815.1	NT	G. lamblia SR2 gene
1767	14357	26903	3.34	2.7E-01	W59087.1	EST_HUMAN	z422h10.11 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:341443 5'
1813	14403	26948	4.14	2.7E-01	P03341	SWISSPROT	GAG POLYPEPTIDE [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2181	15459		2.77	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular monamine transporter type 2, promoter region and exon 1
2405	14973	27545	7.35	2.7E-01	Y13968.1	NT	Feline immunodeficiency virus env gene, isolate ITT0088PIU (M88), partial
2496	15060	27634	3.82	2.7E-01	A1310858.1	EST_HUMAN	ta43c11.x2 NCI_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1 repetitive element
3013	15628		0.73	2.7E-01	BF088284.1	EST_HUMAN	CM1-HT0875-060900-385-605 HT0875 Homo sapiens cDNA
4082	16678	29138	1.98	2.7E-01	A1928015.1	EST_HUMAN	w62e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3'
4096	16891	29147	0.79	2.7E-01	AF218214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
4096	16891	29148	0.79	2.7E-01	AF218214.1	NT	Drosophila buzzatii alpha-esterase 6 (aE6) gene, partial cds
4101	16895	29151	2.31	2.7E-01	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric and
5020	17594	30037	0.98	2.7E-01	L27518.1	NT	Triticum aestivum (Wcs66) gene, complete cds
5193	17758		3.82	2.7E-01	AW866131.1	EST_HUMAN	RC1-CT0286-230200-016-603 CT0286 Homo sapiens cDNA
5471	18105	30424	2.07	2.7E-01	P17277	SWISSPROT	HOMEBOX PROTEIN HOXA4 (CHOX-1.4)
5681	18308		0.98	2.7E-01	AB033171.1	NT	Astropora mytilophthalma mitochondrial cytb gene for cytochrome b, partial cds
6724	18318	32122	1.07	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6724	19318	32123	1.07	2.7E-01	AE001084.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6875	19609	32443	2.03	2.7E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR
7085	19658	32495	0.76	2.7E-01	U15987.1	NT	Drosophila melanogaster rfc40 protein, Rop protein (Rop), and small GTP binding protein (DRas2) genes, complete cds
7393	19918	32782	0.87	2.7E-01	Q11079	SWISSPROT	HYPOPHYSICAL 20.9 KO PROTEIN B0563.3 IN CHROMOSOME X
7562	20079	32854	0.95	2.7E-01	Q01188	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7562	20079	32855	0.95	2.7E-01	Q01188	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7677	20188	33076	2.21	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7677	20188	33077	2.21	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7720	20228	33118	0.92	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' end similar to myosin-binding protein H
7720	20228	33117	0.92	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' end similar to myosin-binding protein H
7805	20348	33256	0.95	2.7E-01	AA013147.1	EST_HUMAN	z35b11.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360957 3' similar to contains Alu repetitive element;
7969	20511		0.51	2.7E-01	AF048820.1	NT	Carassius auratus pituitary adenylate cyclase activating polypeptide type 1 receptor precursor mRNA, complete cds
8079	20821	33534	0.59	2.7E-01	AW888503.1	EST_HUMAN	MR1-SN0062-100500-002-d09 SN0062 Homo sapiens cDNA
8127	20968	33577	0.48	2.7E-01	R39257.1	EST_HUMAN	yc97h06.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:23511 3'
8232	20773	33694	0.94	2.7E-01	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
8894	21233	34154	0.83	2.7E-01	Q14764	SWISSPROT	MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN)
8957	21495	34418	0.53	2.7E-01	X03216.1	NT	Staphylococcus aureus transposon Tn554
9256	21782	34734	9.93	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9256	21782	34735	9.93	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9259	21785		2.02	2.7E-01	P37928	SWISSPROT	FIMBRIAE W PROTEIN
9718	22214	35188	0.87	2.7E-01	D69680.1	NT	Rattus norvegicus DNA for peroxisome assembly factor-2, exon 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 and complete cds
9993	22488	35476	0.91	2.7E-01	AF091848.1	NT	Oryzodagus cucullatus calgranulin C mRNA, partial cds
10028	22521	35517	2.5	2.7E-01	AF087434.1	NT	Mus musculus transcription factor NF-ATc isoform a (NF-ATc) mRNA, complete cds
10148	22643	35634	0.89	2.7E-01	AF156339.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10148	22643	35635	0.69	2.7E-01	AF156339.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10891	23221	36233	2.31	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
10891	23221	36234	2.31	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10702	23231	36244	3.65	2.7E-01	AJ133269.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, DTS522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
12296	24863		1.72	2.7E-01	AB008782.1	NT	Arabidopsis thaliana mRNA for sulfate transporter, complete cds
12501	24627		3.96	2.7E-01	AF217491.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6
495	15416	25615	2.06	2.6E-01	P78411	SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
506	13139		1.24	2.6E-01	D16459.1	NT	Bos taurus mRNA for mb-1, complete cds
1437	14030	26558	2.19	2.6E-01	BE88087.1	EST_HUMAN	801510838F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3812345 5'
1485	14078	26616	1.36	2.6E-01	AB013290.1	NT	Glycine max pseudogene for Bd 30K
1941	14525	27030	6.59	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1941	14525	27081	6.59	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
							bb04d10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2959451 3' similar to gb:M38072 60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14689_cds1 Mouse surfactant protein 3 protein gene (MOUSE);
2140	14718		13.12	2.6E-01	AW733152.1	EST_HUMAN	
2197	14773	27347	1.41	2.6E-01	M11844.1	NT	Human prealbumin gene, complete cds
2512	15076		2.09	2.6E-01	Y12896.1	NT	B. maritimus fbcd. gene
2583	15146		10.77	2.6E-01	BE272440.1	EST_HUMAN	801126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2980043 5'
3640	16243	28719	0.86	2.6E-01	M22342.1	NT	Bacteriophage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds
3705	16306	28775	2.13	2.6E-01	AF229118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
4175	16766	28214	0.7	2.6E-01	AW959510.1	EST_HUMAN	EST371580 IMAGE reserences, MAGF Homo sapiens cDNA
4234	16822	28273	19.98	2.6E-01	BE080598.1	EST_HUMAN	QV1-BT0630-040400-132-903 BT0630 Homo sapiens cDNA
4448	17034	29477	1.57	2.6E-01	AF175293.1	NT	Enterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4593	17176	29822	0.76	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4593	17176	29623	0.76	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4648	17228	29684	1.35	2.6E-01	AA457817.1	EST_HUMAN	aa88d07.r1 Stratiogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838477 5'
4752	17333	29776	1.63	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3*) mRNA, complete cds
4825	17403	29856	1.47	2.6E-01	AF142703.1	NT	Ophrestia radicea maturase-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product
5107	17679	30116	3.56	2.6E-01	H04858.1	EST_HUMAN	y51605.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:152288 5'
5195	17760		0.58	2.6E-01	AA884825.1	EST_HUMAN	am33p11.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1468605 3'
5544	18176		1.29	2.6E-01	AB035972.1	NT	Paramacium caudatum gene for PAP, complete cds
5940	18269	30742	0.68	2.6E-01	M96060.1	NT	Acetobacter xylinum cellulose synthase (bcsA) gene, partial cds, CMCax and CcpAx genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5760	18386		0.81	2.6E-01	A1862398.1	EST_HUMAN	U18603.x1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:2075768 3' similar to contains element MER35 repetitive element ;
5947	18568	31299	0.69	2.6E-01	AF207550.1	NT	Homo sapiens protein translocase, JM26 protein, UDP-galactose translocator, pim-2 protooncogene homolog pim-2h, and shal-type potassium channel genes, complete cds; JM12 protein and transcription factor (GHM enhancer 3 genes, partial cds, and unknown g>
6221	25113		2.36	2.6E-01	AE001811.1	NT	Thermidoga maritima section 123 of 136 of the complete genome
6348	18953	31732	1.89	2.6E-01	A1862557.1	EST_HUMAN	ts02e12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDP1_RAT Q84289 NEUROGENIC DIFFERENTIATION FACTOR 1 ; contains element LTR1 repetitive element ;
6348	18953	31733	1.89	2.6E-01	A1862557.1	EST_HUMAN	ts02e12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDP1_RAT Q84289 NEUROGENIC DIFFERENTIATION FACTOR 1 ; contains element LTR1 repetitive element ;
6554	19152	31948	1.05	2.6E-01	AL162757.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome, segment 877 wd48c04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331368 3' similar to gb:M37721
7103	19873	32512	0.97	2.6E-01	A1914380.1	EST_HUMAN	PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (HUMAN);
7457	24783		0.96	2.6E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome, segment 416
7721	20229	33118	1.6	2.6E-01	R10365.1	EST_HUMAN	y037a03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128004 3' similar to gb:X12517 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
7781	20334	33240	1.14	2.6E-01	R02411.1	EST_HUMAN	y082a07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124212 5'
7845	20387	33280	1.18	2.6E-01	BE144331.1	EST_HUMAN	MRO-H10166-181199-003-012 H10166 Homo sapiens cDNA
8083	20625	33538	0.67	2.6E-01	X82641.1	NT	D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin)
8083	20625	33539	0.67	2.6E-01	X82641.1	NT	D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin)
8278	20817	33738	2.99	2.6E-01	BF343568.1	EST_HUMAN	602014422F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4150366 5'
8349	20890	33810	1.89	2.6E-01	Q10199	SWISSPROT	HYPOTHETICAL 75.2 KD PROTEIN C11G11.02 IN CHROMOSOME II
8627	21166	34080	4.49	2.6E-01	BE830339.1	EST_HUMAN	RC5-E10082-310500-021-F10 ET0082 Homo sapiens cDNA
8627	21166	34081	4.49	2.6E-01	BE830339.1	EST_HUMAN	RC5-E10082-310500-021-F10 ET0082 Homo sapiens cDNA
8388	21811	34762	0.98	2.6E-01	X17604.1	NT	S. occidentalis INV gene for invertase (EC 3.2.1.26)
9654	22153		0.5	2.6E-01	AF057121.1	NT	Lontra canadensis cytochrome b (cyb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
9782	22280	35265	0.93	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KPH-G)
9782	22280	35266	0.93	2.6E-01	P87366	SWISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KPH-G)
10083	22588		0.5	2.6E-01	Q28295	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
10403	22897		0.91	2.6E-01	Y10196.1	NT	Homo sapiens PHEX gene
10500	22894		0.51	2.6E-01	A1878681.1	EST_HUMAN	wr58b09.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2491865 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11300	23752	36809	2.18	2.6E-01	P48280	SWISSPROT	CELL DIVISION PROTEIN FTSW HOMOLOG
11400	23851		30.88	2.6E-01	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
11777	24165		1.72	2.6E-01	10190855	NT	Mus musculus jerky (Jrk), mRNA
11973	24691		4.06	2.6E-01	BE883491.1	EST_HUMAN	601511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3812812 5'
12042	24328	30898	4.8	2.6E-01	AF318898.1	NT	Homo sapiens Na ⁺ /K ⁺ -ATPase gamma subunit (FXYD2) gene, complete cds, alternatively spliced
12396	24556		1.34	2.6E-01	D88425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
12478	24612		1.96	2.6E-01	AE001713.1	NT	Thermoboga maritima section 25 of 136 of the complete genome
12528	24641		1.37	2.6E-01	AF141325.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
12567	24666		3.74	2.6E-01	P47285	SWISSPROT	HYPOTHETICAL PROTEIN MG039
262	12921	25407	1.48	2.5E-01	4502296	NT	Homo sapiens ATP synthase, H ⁺ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
263	12921	25407	1.77	2.5E-01	4502296	NT	Homo sapiens ATP synthase, H ⁺ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
276	12933		4.29	2.5E-01	M26501.1	NT	Starfish (<i>P. ochreus</i>) cytoplasmic actin gene, complete cds
865	13480	25994	1.02	2.5E-01	U06964.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1098	13703		1.03	2.5E-01	AE002156.1	NT	Ureaplasma urealyticum section 57 of 59 of the complete genome
1180	13763	26274	11.59	2.5E-01	T88837.1	EST_HUMAN	ye11g07.11 Stragene lung (#837210) Homo sapiens cDNA clone IMAGE:117468 5'
1566	14158	26689	0.87	2.5E-01	AL115624.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1766	14356		6.09	2.5E-01	4885406	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
1927	15454	27067	1.29	2.5E-01	BE68604.1	EST_HUMAN	PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA
1927	15454	27068	1.29	2.5E-01	BE68604.1	EST_HUMAN	PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA
2452	15019		12.93	2.5E-01	AE000875.1	NT	Aquifex aeolicus section 7 of 109 of the complete genome
2536	15100	27673	0.93	2.5E-01	6678216	NT	Mus musculus protein-L-isocysteine (D-aspartate) O-methyltransferase 1 (Pcmt1), mRNA
2540	15104		1.49	2.5E-01	AA251987.1	EST_HUMAN	EST385464 MAGE resequences, MAGM Homo sapiens cDNA
3459	16066		3.41	2.5E-01	AW973471.1	EST_HUMAN	Danio rerio peptide YY precursor gene, complete cds
3587	16191	28675	0.84	2.5E-01	AF233975.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
3603	16207	28685	7.97	2.5E-01	AL161517.2	NT	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR
4143	16735		1.36	2.5E-01	P32323	SWISSPROT	RHB PROTEIN
4409	16894		0.9	2.5E-01	Q03314	SWISSPROT	Mus musculus neuronal apoptosis inhibitory protein 6 (Naip6) gene, complete cds; and Naip3 gene, exons 2-9 and 11-16
4722	17303	29747	0.59	2.5E-01	AF242431.1	NT	MOLT-INHIBITING HORMONE PRECURSOR (MIH)
4860	17438		1.47	2.5E-01	Q27225	SWISSPROT	

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4888	17445	28888	4.88	2.5E-01	AF007788.1	NT	Choristoneura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds
4898	17471	28927	2.82	2.5E-01	AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 83 of the complete chromosome
4924	17498		3.21	2.5E-01	AJ230113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
4999	17534	29978		2.5E-01	BE898785.1	EST_HUMAN	601437468F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922600 5'
5282	12933		0.81	2.5E-01	M26501.1	NT	Starfish (P. ochreatus) cytoplasmic actin gene, complete cds
5529	18191	30576	12.86	2.5E-01	S83390.1	NT	T3 receptor-associated cofactor-1 [human, fetal liver, mRNA, 2830 nt]
6114	18730		0.84	2.5E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6738	19332	32138	0.83	2.5E-01	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
7389	19914	32778	0.82	2.5E-01	U13892.1	NT	Feline calicivirus CFI/68 RNA helicase/cysteine protease/RNA-dependent RNA polymerase polypeptide precursor and capsid protein precursor, genes, complete cds; and unknown gene
7413	19938		1.35	2.5E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
7632	20144	33025	4.48	2.5E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
7788	20329	33238	2.31	2.5E-01	BF109040.1	EST_HUMAN	7157403.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3526389 3'
7797	20340	33248	0.7	2.5E-01	BE960712.1	EST_HUMAN	60165339 IR2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826188 3'
8188	20709	33623	2.2	2.5E-01	BF038595.1	EST_HUMAN	601458238F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3682809 5'
8336	20877	33798	0.72	2.5E-01	P04492	SWISSPROT	E1B PROTEIN, SMALL T-ANTIGEN (E1B 18K)
8571	21110	34029	3.03	2.5E-01	H53238.1	EST_HUMAN	XQ8407.1 Soares fetal liver spleen TNF- α Homo sapiens cDNA clone IMAGE:202501 5'
8808	21347	34271	0.88	2.5E-01	M88628.1	NT	Mouse testis-specific protein (TPX-1) gene, exon 10
9435	21891	34909	15.98	2.5E-01	U86631.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9435	21881	34910	15.98	2.5E-01	U86631.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9492	21948	34897	2.09	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
9492	21948	34898	2.09	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
10010	22505	35498	1.66	2.5E-01	AW581987.1	EST_HUMAN	RC3-ST0188-130100-018-e07 ST0188 Homo sapiens cDNA
10438	22930						XG40c10.x1 NCI_CGAP_UH Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element/contains element MSR1 repetitive element
10438	22930	35937	1.53	2.5E-01	AW152248.1	EST_HUMAN	
10439	22933	35941	1.31	2.5E-01	X58491.1	NT	Mouse L1Md LINE DNA
10459	22953	35962	2.03	2.5E-01	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
10459	22953	35963	2.03	2.5E-01	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
10955	23470	36495	4.3	2.5E-01	D50914.1	NT	Human mRNA for KIAA0124 gene, partial cds
11712	24122	37153	5.29	2.5E-01	AF200528.1	NT	Zea mays cellulose synthase-4 (Csa-4) mRNA, complete cds
11740	25075		10.13	2.5E-01	AL161541.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41
579	13208	25887	1.87	2.4E-01	AA836318.1	EST_HUMAN	on70d04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'
881	13495	26014	2.4	2.4E-01	BF76124.1	EST_HUMAN	602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5'

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1347	13942	26464	21.36	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1347	13942	26465	21.36	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1427	14020	26548	0.93	2.4E-01	Y17280.1	NT	Homo sapiens FLI-1 gene, partial
1891	14476		27.27	2.4E-01	AF267753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds
1944	14528	27084	1.17	2.4E-01	AF251708.1	NT	Zaocys thumnae fructose-1,6-bisphosphatase mRNA, complete cds
2079	14659	27230	1.49	2.4E-01	AJ742958.1	EST_HUMAN	wg78405.x1 Soares, NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371017 3' similar to TR:060267 O60267 KIAA0512 PROTEIN.
2183	14759	27329	1.04	2.4E-01	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
2213	14788		1.04	2.4E-01	P45384	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE)
2302	14875	27451	1.78	2.4E-01	AE000880.1	NT	Aquifex aeolicus section 12 of 109 of the complete genome
2425	14993	27586	1.26	2.4E-01	BF002171.1	EST_HUMAN	7h23d04.x1 NCI CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW:PRSB_XENLA
2575	15138	27708	3.05	2.4E-01	Z38534.1	NT	O42598 265 PROTEASE REGULATORY SUBUNIT 8A.
2790	15343	27913	1.79	2.4E-01	X71783.1	NT	D.discoideum (Ax3-K) panA gene
2812	15364	27933	3.88	2.4E-01	AF030154.1	NT	S.pombe swi6 gene
3166	15780		3.27	2.4E-01	U72726.1	NT	Bovine adenovirus 3 complete genome
3182	15795	28267	1.38	2.4E-01	X74209.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pol) genes, complete cds
3724	16325	28792	1.26	2.4E-01	AF169793.1	NT	H.sapiens AGT gene, PstI fragment of intron 4
3824	16424	28886	0.83	2.4E-01	AE000312.1	NT	Podospira anserina HET-C protein (Het-c) gene, complete cds
4103	16697		0.6	2.4E-01	D28960.1	NT	Escherichia coli K-12 MG1685 section 202 of 400 of the complete genome
5008	17581	30024	1.08	2.4E-01	AE000305.1	NT	Rattus norvegicus mRNA for alphaB crystallin-related protein, complete cds
5220	17785	30203	0.93	2.4E-01	BE737592.1	EST_HUMAN	Escherichia coli K-12 MG1685 section 195 of 400 of the complete genome
5302	17864		1.55	2.4E-01	K02402.1	NT	601572862F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839775 5'
5653	18280	30758	0.83	2.4E-01	A1925707.1	EST_HUMAN	Human coagulation factor IX gene, complete cds
5653	18280	30759	0.83	2.4E-01	A1925707.1	EST_HUMAN	wc33405.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5676	18303	30785	0.85	2.4E-01	D50871.1	NT	wc33405.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5836	18460	31182	7.92	2.4E-01	AF091216.1	NT	Glycine max mRNA for mitotic cyclin b1-type, complete cds
5836	18460	31183	7.92	2.4E-01	AF091216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds
6050	24754		1.02	2.4E-01	AJ133836.2	NT	Mus musculus Wm protein (Wm) gene, complete cds
							Branchiostoma floridae mRNA for calmodulin 2 (calM2 gene)
6054	18672	31411	2.36	2.4E-01	BF592336.1	EST_HUMAN	7154d04.x1 NCI CGAP_Br18 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW:SFR4_HUMAN
6138	18752	31510	2.5	2.4E-01	AF035546.1	NT	Q08170 SPLICING FACTOR, ARGinine/SERINE-RICH 4 ;contains element TAR1 TAR1 repetitive element
							Drosophila melanogaster p38a MAP kinase gene, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6240	18949	31619	2.26	2.4E-01	7661801	NT	Homo sapiens HSPC142 protein (HSPC142), mRNA
6290	18898	31609	0.8	2.4E-01	AV733787.1	EST_HUMAN	AV733787 cDNA Homo sapiens cDNA clone cdaADE11 5'
6656	19252	32055	2.43	2.4E-01	AI698989.1	EST_HUMAN	wc82c11.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:232320 3' similar to gb:J03484
7381	19907	32772	8.84	2.4E-01	L43001.1	EST_HUMAN	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
7709	20218	33106	1.06	2.4E-01	AF229644.1	NT	Bos taurus guanylyl cyclase-activating protein 2 (guca2) mRNA, complete cds
8139	20680	33591	0.71	2.4E-01	AJ006397.1	NT	Mus musculus DXImx48e protein (DXImx48e) mRNA, complete cds
8139	20680	33592	0.71	2.4E-01	AJ006397.1	NT	Streptococcus pneumoniae r08 and h08 genes; two component system 08
8290	20831	33752	1.86	2.4E-01	AJ012585.1	NT	Streptococcus pneumoniae r08 and h08 genes; two component system 08
8335	21074	33964	0.97	2.4E-01	BF24794.1	EST_HUMAN	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2
8588	21127		0.58	2.4E-01	BF78275.1	EST_HUMAN	60187767F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106298 5'
9059	21596	34526	0.58	2.4E-01	AL139077.2	NT	602088188F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250372 5'
9059	21596	34527	0.58	2.4E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
9482	21881	34826	6.84	2.4E-01	AI693515.1	EST_HUMAN	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
9620	22120	35083	0.6	2.4E-01	AF220067.1	NT	w443602.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330906 3' similar to contains
9620	22120	35084	0.6	2.4E-01	AF220067.1	NT	MER22.b1 TAR1 repetitive element
10335	22829	35823	1.95	2.4E-01	Q03692	SWISSPROT	Drosophila melanogaster SKPB gene, complete cds
10847	23179	36192	3.25	2.4E-01	AL161494.2	NT	Drosophila melanogaster SKPB gene, complete cds
10715	23243	36260	2.9	2.4E-01	AF030199.1	NT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
11081	23593		2.28	2.4E-01	Z21647.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
11695	24089	37145	1.91	2.4E-01	AF217491.1	NT	Mus musculus type 1 sigma receptor gene, complete cds
11807	24853		2.65	2.4E-01	AF004213.1	NT	P. asiatica mosaic virus genomic RNA
11866	24220		2.02	2.4E-01	AJ278191.1	NT	Homo sapiens fragile 18D oxidoreductase (FOR) gene, exon 6
12086	24838		2.18	2.4E-01	V01507.1	NT	Arabidopsis thaliana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds
12320	25081		1.5	2.4E-01	BF229975.1	EST_HUMAN	Mus musculus mRNA for putative mc7 protein (mc7 gene)
12582	24662		2.31	2.4E-01	AL163281.2	NT	Gallus gallus gene coding for e-actin
412	13047	25538	0.91	2.3E-01	S75898.1	NT	RC3-CT0413-100800-023-506 CT0413 Homo sapiens cDNA
665	13289		4.4	2.3E-01	U9713.1	NT	Homo sapiens chromosome 21 segment HS21C081
695	13318	25903	17.02	2.3E-01	U87596.1	NT	aromatase [Poephila guttata=zabira finches, ovary, mRNA, 3188 nt]
969	13560	26092	3.44	2.3E-01	BE311893.1	EST_HUMAN	Myoplasma genitalium section 35 of 51 of the complete genome
1647	14239	26774	1.19	2.3E-01	AJ254580.1	NT	Methanococcus jannaschii section 138 of 150 of the complete genome
1674	14266	26800	2.75	2.3E-01	Y10887.2	NT	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505618 5'
2089	14669		1.28	2.3E-01	AJ233353.1	NT	Brassica napus sfg gene for S-lucis glycoprotein, cultivar T2
							Mus musculus cdh5 gene, exon 1, partial
							Homo sapiens partial intron 3 of the wild type AF-4/FEL gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2489	15054	27626	2.03	2.3E-01	BE297718.1	EST_HUMAN	601175562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'
2878	15236	27803	1.16	2.3E-01	M11319.1	NT	Human erythropoietin gene, complete cds
2851	14024	26552	1.42	2.3E-01	AB015033.1	NT	Marriliabilla agarivorans gyrB gene for DNA gyrase subunit B, partial cds, strain:IFO 14957
2990	15606	28086	0.93	2.3E-01	AA601379.1	EST_HUMAN	no16d08.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu repetitive element; contains element THR repetitive element
3120	15734		6.96	2.3E-01	R21732.1	EST_HUMAN	yt21b07.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3'
3417	16025	28507	0.78	2.3E-01	H69836.1	EST_HUMAN	yt97h10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213283 5'
3908	16507	28969	1.02	2.3E-01	S82821.1	NT	GSTA5=glutathione S-transferase Yc2 subunit (5' region, intron 1) [rats, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3]
4009	16607		5.14	2.3E-01	7862133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4442	17028	29468	0.83	2.3E-01	R82252.1	EST_HUMAN	yt17f01.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149017 5'
4489	17074		2.4	2.3E-01	L78789.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4548	17131	29578	0.87	2.3E-01	D90899.1	NT	Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
4588	17169	29613	2.18	2.3E-01	AF092535.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
4652	17234	29690	6.13	2.3E-01	5031984	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
5180	17585	30028	0.62	2.3E-01	J03280.1	NT	Human phenylethanolamine N-methyltransferase gene, complete cds
5202	17767	30191	0.62	2.3E-01	AB032400.1	NT	Mus musculus tulip 1 mRNA, complete cds
5403	17961	30372	0.9	2.3E-01	AE000240.1	NT	Escherichia coli K-12 MG1655 section 130 of 400 of the complete genome
5507	18140	30552	2.39	2.3E-01	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
5621	18250	30718	2.05	2.3E-01	BF058381.1	EST_HUMAN	7k30b08.x1 NCL_CGAP_OV18 Homo sapiens cDNA clone IMAGE:3476698 3' similar to SW:GAG_SMSAV P03330 GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10] ;
5721	18347	31050	4.58	2.3E-01	X96587.1	NT	C. familiaris rom1 gene
5831	18455		1.19	2.3E-01	L39112.1	NT	Vitellogenin small subunit ribosomal RNA gene
5826	18548	31274	0.78	2.3E-01	S60371.1	NT	23S rRNA [Leuconostoc carnosum, Genomic, 2866 nt]
6096	18712	31461	2.34	2.3E-01	A1708840.1	EST_HUMAN	as27e12.x1 Barstead aorta HPLR86 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238
6096	18712	31462	2.34	2.3E-01	A1708840.1	EST_HUMAN	as27e12.x1 Barstead aorta HPLR86 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:X13238
6762	19355	32184	0.76	2.3E-01	AF198089.1	NT	Cytocb1egus cuniculus cytochrome oxidase subunit VIa (coxVIa2) mRNA, complete cds; nuclear gene for mitochondrial product
6959	19536	32380	4.1	2.3E-01	A1718148.1	EST_HUMAN	as42f12.x1 Barstead aorta HPLR86 Homo sapiens cDNA clone IMAGE:2318887 3' similar to contains Alu repetitive element;
7165	19697	32544	0.7	2.3E-01	8923323	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7331	19858	32721	0.89	2.3E-01	AF000227.1	NT	Secale cereale omega secalin gene, complete cds
7445	19989	32837	2.42	2.3E-01	AF175389.1	NT	Glycine max resistance protein LM17 precursor RNA, partial cds
7603	20116		3.63	2.3E-01	8754779	NT	Mus musculus myosin XV (Myo15), mRNA
7608	20121	32898	1.63	2.3E-01	BE888071.1	EST_HUMAN	601511573F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912859 5'
7732	20240		2.68	2.3E-01	N80983.1	EST_HUMAN	zai12e08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:282358 5'
7763	20336	33243	0.58	2.3E-01	AL161558.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58
7835	20477	33387	1.93	2.3E-01	M68831.1	NT	Oxytricha nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds
8430	20970	33882	0.9	2.3E-01	U57969.1	NT	Mus musculus prosaposin (psap)(SQP-1) gene, complete cds
9087	21604	34534	0.87	2.3E-01	AA372164.1	EST_HUMAN	EST84061 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X633388)
9087	21604	34535	0.87	2.3E-01	AA372164.1	EST_HUMAN	EST84061 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X633388)
9501	22001	34938	0.65	2.3E-01	6078318	NT	Mus musculus phosphatidylinositol 3-kinase catalytic subunit delta (Pik3cd), mRNA
9644	22144	35112	0.51	2.3E-01	BE277860.1	EST_HUMAN	601120110F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2868739 5'
9697	22166	35169	0.76	2.3E-01	AW964460.1	EST_HUMAN	EST376533 MAGE resequences, MAGH Homo sapiens cDNA
9748	22244	35225	1.22	2.3E-01	X52124.1	NT	Haemophilus influenzae genes for HincII restriction-modification system (HincII methyltransferase (EC 2.1.1.72) and HincII endonuclease (EC 3.1.21.4))
9781	22278	35284	0.55	2.3E-01	AW364633.1	EST_HUMAN	PM2-DT0036-281289-001-104 DT0036 Homo sapiens cDNA
9847	22345	35326	2.6	2.3E-01	BE173060.1	EST_HUMAN	MRO-HT0558-240400-014-g11 HT0559 Homo sapiens cDNA
9903	22400	35373	1.93	2.3E-01	AJ293261.1	NT	Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes
10339	22833	35828	0.94	2.3E-01	AF201929.1	NT	Murine hepatitis virus strain 2, complete genome
10351	22845		5.86	2.3E-01	BF133577.1	EST_HUMAN	601846159R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102092 3'
10893	23414	36432	1.85	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
10893	23414	36433	1.85	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
11088	23580	36619	1.85	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11088	23580	36620	1.85	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11230	23761	36817	2.49	2.3E-01	AE002167.2	NT	Chlamydia pneumoniae AR39, section 4 of 94 of the complete genome
11624	24066		1.6	2.3E-01	AV709738.1	EST_HUMAN	AV709736 ADC Homo sapiens cDNA clone ADCAGH01 5'
11788	24172		2.82	2.3E-01	U45428.1	NT	Borrelia burgdorferi 2.9-6 locus, ORF A-D genes, complete cds and REP+ gene, partial cds
11878	24226		57.94	2.3E-01	T27231.1	EST_HUMAN	HCOEST44 HT29M6 Homo sapiens cDNA clone HCOE44 5'
11899	24804		1.31	2.3E-01	AA089819.1	EST_HUMAN	chm1424.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
11908	24246		1.61	2.3E-01	AW863940.1	EST_HUMAN	PM4-SN0012-030400-001-b06 SN0012 Homo sapiens cDNA
11989	25002	30610	3.1	2.3E-01	AW303623.1	EST_HUMAN	x21d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR-Q9Z175 Q9Z175 LYSYL OXIDASE-RELATED PROTEIN 2, contains P.TRS.b2 TAR1 repetitive element;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12007	25053	30511	10.96	2.3E-01	BE882464.1	EST_HUMAN	601507202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3809689 5'
12057	24340		1.94	2.3E-01	BF663319.1	EST_HUMAN	602144459F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297719 5'
12107	24369		3.11	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12205	24429		1.36	2.3E-01	U49845.1	NT	Pleurodeles waltl distal-less like protein PwDlx-3 (PwDlx-3) mRNA, complete cds
12211	24369		1.67	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12480	24614		2.57	2.3E-01	BF475611.1	EST_HUMAN	nac39h12.x1 Lupski_sciatic_nerve Homo sapiens cDNA clone IMAGE:3395950 3' similar to contains element
12668	24868	30710	1.26	2.3E-01	AA094108.1	EST_HUMAN	MER38 repetitive element
93	12769	26252	0.91	2.2E-01	AJ052190.1	EST_HUMAN	cl1864.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
1611	14204	26738	2.85	2.2E-01	AF187650.1	NT	oz14a10.x1 Scarses fetal, liver, spleen, 1NFLS, S1 Homo sapiens cDNA clone IMAGE:1675290 3' similar to
2063	14643	27287	3.89	2.2E-01	AF171901.1	NT	TR.Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN
2136	14714	27287	3.16	2.2E-01	M34640.1	NT	Homo sapiens PPAR delta gene, promoter region
2447	15014	27586	5.61	2.2E-01	BF677538.1	EST_HUMAN	Trimerus malabaricus cyb gene, partial cds; mitochondrial gene for mitochondrial product
2623	15185	27751	1.27	2.2E-01	BE616258.1	EST_HUMAN	Fresh-water sponge Emf1 alpha collagen (COLF1) gene
2623	15185	27752	1.27	2.2E-01	BE616258.1	EST_HUMAN	602085608F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4246989 5'
2703	15260		1.17	2.2E-01	AL163218.2	NT	601462628F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866180 5'
2906	15523	27993	4.28	2.2E-01	BE156625.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C018
2906	15523	27994	4.28	2.2E-01	BE156625.1	EST_HUMAN	PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA
2947	15563		1.64	2.2E-01	AF020503.1	NT	PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA
3439	16047		2.67	2.2E-01	AL161562.2	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
3686	16484		1.18	2.2E-01	AF155728.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62
4291	16877		1.28	2.2E-01	AF119102.1	NT	Xiphophorus maculatus truncated Rex1 retrotransposon reverse transcriptase (RT) pseudogene
4300	16886	29330	7.03	2.2E-01	AF155142.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4350	16937	29378	2.59	2.2E-01	AF117340.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
4350	16937	29378	2.59	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mek1) mRNA, complete cds
4447	17033	29475	1.36	2.2E-01	U01307.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mek1) mRNA, complete cds
4447	17033	29476	1.36	2.2E-01	U01307.1	NT	Human scRNA (BC200 beta) pseudogene
4952	17527		1.35	2.2E-01	D50604.1	NT	Human scRNA (BC200 beta) pseudogene
4957	17532	29974	2.86	2.2E-01	AA211216.1	EST_HUMAN	Human beta-cytoplasmic actin (ACTBP9) pseudogene
5196	17761		1.33	2.2E-01	U13299.1	NT	z87c05.r1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:648968 5'
5203	17768		1.79	2.2E-01	AE001137.1	NT	Mus musculus vinculin gene, exon 3
							Borrelia burgdorferi (section 23 of 70) of the complete genome

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5291	17853	30277	1.2	2.2E-01	BE141035.1	EST_HUMAN	MRO-HT0067-201099-002-c10 HT0087 Homo sapiens cDNA
5316	17878		0.9	2.2E-01	S57565.1	NT	histamine H2-receptor [rats, Genomic, 1928 nt]
5919	18541	31267	2.46	2.2E-01	5803002	NT	Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 156, mRNA
5930	18552		3.53	2.2E-01	D64000.1	NT	Synechocystis sp. PCC6803 complete genome, 19/27, 2392729-2538999
6150	18763	31525	0.73	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-Tbx1) mRNA, complete cds
6150	18763	31528	0.73	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-Tbx1) mRNA, complete cds
6807	19398	32212	0.85	2.2E-01	AB038490.1	NT	Homo sapiens gene for fukutin, complete cds
7093	19684	32503	9.14	2.2E-01	AV756238.1	EST_HUMAN	AV756238 BM Homo sapiens cDNA clone BMFAHC06 5'
7183	18715	32562	1.46	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphotyrosyl-tyrosophosphatase synthase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes
7183	18715	32563	1.46	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphotyrosyl-tyrosophosphatase synthase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes
7333	18860	32723	2.01	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7333	18860	32724	2.01	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7688	20197	33085	0.88	2.2E-01	AF287967.1	NT	Homo sapiens homeobox B7 (HOXB7) gene, partial cds; and homeobox B6 (HOXB6), homeobox B5 (HOXB5), homeobox B4 (HOXB4), and homeobox B3 (HOXB3) genes, complete cds
7863	20505		3.06	2.2E-01	AF155143.1	NT	Mus musculus nm23-M1 gene, promoter region
8032	20574	33479	0.84	2.2E-01	Z48633.1	NT	E coli sepA and sepB genes
8815	21354	34277	0.57	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds
8815	21354	34278	0.57	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds
8827	21366	34290	3.48	2.2E-01	AE001713.1	NT	Thermoplasma maritima section 25 of 136 of the complete genome
8847	21386	34310	1.02	2.2E-01	U09964.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
8952	21490		3.12	2.2E-01	AW855039.1	EST_HUMAN	PX3-CT0263-241289-009-b07 CT0263 Homo sapiens cDNA
9043	21580	34509	1.82	2.2E-01	8393247	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Dearf1), mRNA
9128	21661	34604	1.95	2.2E-01	BF376354.1	EST_HUMAN	MRI-TN0045-110900-006-c02 TN0045 Homo sapiens cDNA
9213	21730	34673	1.24	2.2E-01	W02888.1	EST_HUMAN	z04008.r1 Soares melanocyte 2Nbl-M Homo sapiens cDNA clone IMAGE:281991 5'
9231	21853	34603	14.03	2.2E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9274	21800	34750	0.74	2.2E-01	AJ009839.1	NT	Xenopus laevis mRNA for kinesin-like protein 3 (xklp3)
9285	21885	34830	0.71	2.2E-01	7657428	NT	Mus musculus osteoblast specific factor 2 (OSF-2), mRNA
9288	21888	34845	3.69	2.2E-01	M8643.1	NT	Brachydanio rerio epandrin beta and gamma chains (Epd) gene, complete cds
9539	22039	35000	0.99	2.2E-01	Q90980	SWISSPROT	CYCLIC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CNG-3) (CNG3)

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9729	22227	35204	3.1	2.2E-01	AF197941.1	NT	Funaria hygrometrica chloroplast-localized small heat shock protein (CPsHSP21) mRNA, complete cds;
9864	22361	35341	2.23	2.2E-01	BF206507.1	EST_HUMAN	nuclear gene for chloroplast product
10079	22574	35569	0.87	2.2E-01	9625671	NT	601869724F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5'
10340	22834		0.61	2.2E-01	AF071001.1	NT	Human herpesvirus 5, complete genome
10384	22878	35870	0.72	2.2E-01	AE001562.1	NT	Mus musculus PHR1 (Phr1) gene, partial cds
10384	22878	35871	0.72	2.2E-01	AE001562.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
11005	23519	36554	1.6	2.2E-01	AF257772.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
11298	23751	36808	5.56	2.2E-01	X01918.1	NT	Homo sapiens RNA binding protein MCG10 gene, complete cds, alternatively spliced
11335	23033	36042	3.18	2.2E-01	7708215	NT	Drosophila 68G glue gene cluster
11715	24125		1.8	2.2E-01	BE87059.1	EST_HUMAN	Homo sapiens H-2K binding factor-2 (LOC51580), mRNA
11827	25065		6.34	2.2E-01	U82671.2	NT	601446957F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850670 5'
11910	24248		5.37	2.2E-01	AF189843.1	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), calretinin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
12024	18029	30491	1.7	2.2E-01	AW361098.1	EST_HUMAN	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
12025	24317		1.85	2.2E-01	AW661922.1	EST_HUMAN	RC1-CT0249-141199-021-g04 CT0249 Homo sapiens cDNA
12575	25058		4.05	2.2E-01	AV694801.1	EST_HUMAN	h17502.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972523 3'
12659	24730	30855	2.44	2.2E-01	BF243065.1	EST_HUMAN	AV694801 GKG Homo sapiens cDNA clone GKCAB02 5'
1006	13617	26132	1.36	2.1E-01	AA569289.1	EST_HUMAN	601876452F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104996 5'
1009	13619	26134	1.27	2.1E-01	AL161504.2	NT	nm31e11.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1061804
1163	13765		2.41	2.1E-01	AE002314.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
1240	13838	26354	0.85	2.1E-01	6754299	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1240	13838	26355	0.85	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1557	14149	26581	3.45	2.1E-01	AJ249895.1	NT	Mus musculus mas proto-oncogene and Igf2r gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes
1957	14541	27097	1.84	2.1E-01	AA906824.1	EST_HUMAN	ok73402.s1 NCI_CGAP_G04 Homo sapiens cDNA clone IMAGE:1519810 3' similar to gb:K02765
2201	14777	27350	3.39	2.1E-01	BF695073.1	EST_HUMAN	COMPLEMENT C3 PRECURSOR (HUMAN);
2385	14954	27526	2.01	2.1E-01	6753235	NT	602083129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5'
2951	15567	28041	2.53	2.1E-01	6912445	NT	Mus musculus calcium channel, voltage dependent, alpha2/delta subunit 3 (Cacna2d3), mRNA
3879	16477		6.58	2.1E-01	9838361	NT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
4129	16721	29176	1.22	2.1E-01	P11675	SWISSPROT	Beta vulgaris mitochondrion, complete genome
							IMMEDIATE-EARLY PROTEIN IE180

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4129	16721	29177	1.22	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4336	16923		1.38	2.1E-01	AF124526.1	NT	Orchesta cavimana calcium-binding protein BP23 precursor (BP23) gene, complete cds
4465	17051		1.51	2.1E-01	AB033041.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
4876	17258	29709	1.83	2.1E-01	AB010273.1	NT	Homo sapiens pshp47 gene, complete cds
5083	17658	30097	1.63	2.1E-01	U78409.1	NT	Lycopodium esculentum homeobox 1 protein (THox1) mRNA, partial cds
5434	17990	30396	0.99	2.1E-01	J05082.1	NT	Vampire bat (D. rotundus) plasminogen activator mRNA, complete cds
5504	18138	30548	6.55	2.1E-01	BF672695.1	EST_HUMAN	602152001F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293001 5'
6987	19544	32368	1.16	2.1E-01	AJ223392.1	NT	Dodo fragilis mitochondrial 16S rRNA gene, partial
6979	19477	32299	2.04	2.1E-01	U04642.1	NT	Human olfactory receptor (OR17-2) gene, partial cds
7436	19960	32825	1.24	2.1E-01	Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7436	19960	32826	1.24	2.1E-01	Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7447	19971		2.17	2.1E-01	AE000972.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
7692	20201	33088	2.02	2.1E-01	AF000949.1	NT	Canis familiaris keratin (KRT19) gene, complete cds
7731	20239	33130	1.14	2.1E-01	AF068687.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
7731	20239	33131	1.14	2.1E-01	AF068687.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
7765	20273		0.68	2.1E-01	T87354.1	EST_HUMAN	y483b01.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:114793 5'
8017	20559		1.19	2.1E-01	7305030	NT	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.1b), mRNA
8439	20979	33894	4.93	2.1E-01	U66399.1	NT	Haemophilus influenzae hmcD, putative haemocin processing protein (hmcC), putative ABC transporter (hmcB), putative haemocin structural protein (hmcA), and haemocin immunity protein (hmcI) genes, complete cds
8732	21271	34190	0.82	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0814_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H0814 5'
8732	21271	34191	0.82	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0814_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H0814 5'
8888	21426		0.47	2.1E-01	AB022524.1	NT	Homo sapiens APC gene, exon 9
8967	21505	34428	5.93	2.1E-01	Z35766.1	NT	S. cerevisiae chromosome II reading frame ORF YBL025w
9423	21932	34880	0.6	2.1E-01	N42536.1	EST_HUMAN	y11e10.r1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:270854 5'
9423	21932	34881	0.6	2.1E-01	N42536.1	EST_HUMAN	y11e10.r1 Soares melanocyte 2N8HM Homo sapiens cDNA clone IMAGE:270854 5'
9432	21958	34906	2.95	2.1E-01	X97378.1	NT	A. thaliana mRNA for AtRanBP1b protein
9536	22036	34986	1.57	2.1E-01	AB038529.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 6
10232	22727	35719	1.04	2.1E-01	Z97087.1	NT	Beta vulgaris mRNA for elongation factor 1-beta
10263	22758	35745	1.96	2.1E-01	P52824	SWISSPROT	DIACYLGLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA)
10268	22764	35751	0.67	2.1E-01	BF574254.1	EST_HUMAN	602131427F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270831 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10505	22999	36007	0.5	2.1E-01	AF294296.1	NT	Anolis lineatopus isolate NG NADH dehydrogenase subunit 2 (ND2) gene, complete cds, mitochondrial gene for mitochondrial product
11438	23898		2.24	2.1E-01	11036647	NT	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA
11451	23901	38969	2.34	2.1E-01	BE180422.1	EST_HUMAN	RC3-H10622-040500-013.b11 HT0622 Homo sapiens cDNA
11641	24602		1.39	2.1E-01	X57824.1	NT	Drosophila melanogaster ALA-E6 DNA, repeat region
12183	24418		1.48	2.1E-01	AF217490.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds
12465	24593		1.72	2.1E-01	BE622149.1	EST_HUMAN	801440712F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915675 5'
12607	24691	30858	2.08	2.1E-01	BE672330.1	EST_HUMAN	7a59e02.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:3223034 3'
12612	24695	30861	1.28	2.1E-01	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
214	12875	25382	1.86	2.0E-01	AB017437.1	NT	Gallus gallus mRNA for avian, complete cds
559	13190		2.2	2.0E-01	7705801	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
728	13348	25840	1.24	2.0E-01	M77085.1	NT	O cuniculus germline IgH heavy chain V-H pseudogene, allotype V-Ha2
843	13459	25968	1.76	2.0E-01	AF072865.1	NT	Mus musculus Major Histocompatibility Locus class II region
1049	13656	26167	0.72	2.0E-01	D90905.1	NT	Synochocytis sp. PCC6803 complete genome, 7/27, 761449-920915
1164	13766	26276	3.24	2.0E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1297	13891	26414	1.37	2.0E-01	AJ132695.5	NT	Homo sapiens rec1 gene
1351	13946	26470	1.22	2.0E-01	AW384937.1	EST_HUMAN	PM1-HT0422-291299-002-c06 HT0422 Homo sapiens cDNA
1507	14099		1.22	2.0E-01	AJ243957.1	NT	Plum pox virus strain M, complete genome, isolate PS
1534	14126	26663	23.08	2.0E-01	4503408	NT	Homo sapiens dystrobrevin, alpha (DTNA), mRNA
1599	14191	26722	3.03	2.0E-01	AB007974.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505
1604	14196	26728	1.23	2.0E-01	AF260700.1	NT	Homo sapiens sodium/iodide symporter mRNA, partial cds
1735	14326	26868	1.17	2.0E-01	U22346.1	NT	Human bradykinin B1 receptor (bradyb1) gene, complete cds
1755	14345		1.83	2.0E-01	AF111170.3	NT	Homo sapiens 14q32 jagged2 gene, complete cds, and unknown gene
1795	14385		1.99	2.0E-01	U67525.1	NT	Methanococcus jannaschii section 87 of 150 of the complete genome
1834	14518	27073	1.14	2.0E-01	BE871330.1	EST_HUMAN	801449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
1934	14518	27074	1.14	2.0E-01	BE871330.1	EST_HUMAN	801449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
1937	14521	27077	1	2.0E-01	8922238	NT	Homo sapiens hypothetical protein FLJ10120 (FLJ10120), mRNA
2386	14955		1.64	2.0E-01	X62877.1	NT	H. sapiens Na+-D-glucose cotransport regulator gene
2915	15532		0.68	2.0E-01	AF074990.1	NT	Homo sapiens full length insert cDNA YH85A11
3534	16139	28621	0.7	2.0E-01	P46807	SW/ISSPROT	HOMEOBOX PROTEIN GLABRA2 (HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
3626	16229		0.82	2.0E-01	AW238005.1	EST_HUMAN	xp15602.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element MER21 repetitive element
3768	16369	28835	0.8	2.0E-01	P34641	SW/ISSPROT	GED-11 PROTEIN

Table 4

Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4028	16626	28098	0.78	2.0E-01	Z46906.1	NT	<i>Sus scrofa</i>
4102	16696	29152	0.68	2.0E-01	X83997.1	NT	<i>C.parasitica</i> eapC gene
4522	17106	29552	0.76	2.0E-01	AF242431.1	NT	<i>Mus musculus</i> neuronal apoptosis inhibitory protein 6 (Naip6) gene, complete cds; and Naip3 gene, exons 2-9 and 11-16
4665	17247		8.43	2.0E-01	BE826165.1	EST_HUMAN	QV4-EN0032-190500-223-e03 EN0032 Homo sapiens cDNA
5192	17757	30186	7.09	2.0E-01	8922080	NT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
5226	16139	28621	0.62	2.0E-01	P46907	SWISSPROT	HOMEOBOX PROTEIN GLABRA2 (HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
5636	18265	30737	2.38	2.0E-01	X68600.1	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5916	18538	31283	2	2.0E-01	11432540	NT	Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA
6008	18626	31361	0.69	2.0E-01	X91856.1	NT	<i>F.rubripes</i> DNA encoding for vail-RNA synthetase
6210	18820	31591	6.48	2.0E-01	U15300.1	NT	<i>Saccharomyces cerevisiae</i> Hal5p (HAL5) mRNA, complete cds
6321	18928		0.71	2.0E-01	M75967.1	NT	Human hepatocyte growth factor gene, exon 1
6560	19158	31955	3.94	2.0E-01	X61033.1	NT	<i>M.aureus</i> mu class glutathione transferase gene
6650	19246	32049	3.63	2.0E-01	AW360865.1	EST_HUMAN	PM1-CT0247-141089-001-g06 CT0247 Homo sapiens cDNA
7251	19780	32636	0.88	2.0E-01	U39724.1	NT	<i>Mycoplasma genitalium</i> section 46 of 51 of the complete genome
7336	18863	32727	1.18	2.0E-01	AF260371.1	NT	<i>Mus musculus</i> phosphofructokinase-1 C isozyme (Pfkfb) gene, exons 3 through 7
7775	20284	33181	1.53	2.0E-01	AK024427.1	NT	Homo sapiens mRNA for FLJ000119 protein, partial cds
7895	20437		6.45	2.0E-01	AF028026.1	NT	Andes virus strain Q123133 glycoprotein G1 and G2 precursor, gene, partial cds
8142	20683	33595	2.91	2.0E-01	X81151.1	NT	<i>M.musculus</i> scp2 gene exon 14
8658	21187		0.53	2.0E-01	BE562247.1	EST_HUMAN	601344848F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE3677794 5'
9273	21799	34749	1.03	2.0E-01	U82511.1	NT	<i>Diclypsellium discoidium</i> random slug cDNA19 protein (sc19) mRNA, partial cds
9312	21826	34775	0.65	2.0E-01	U71122.1	NT	<i>Arabidopsis thaliana</i> pyruvate decarboxylase-2 (Pdc2) gene, complete cds
9475	21874		4.35	2.0E-01	AE001278.1	NT	<i>Chlamydia trachomatis</i> section 5 of 87 of the complete genome
9681	22190	35132	0.51	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
9681	22160	35133	0.51	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
9809	22304		1.98	2.0E-01	AF146982.1	NT	Homo sapiens filamin 2 (FLN2) mRNA, complete cds
9854	22449	35431	1.79	2.0E-01	AF086907.1	NT	<i>Arabidopsis thaliana</i> root gravitropism control protein (PIN2) gene, complete cds
9854	22449	35432	1.79	2.0E-01	AF086907.1	NT	<i>Arabidopsis thaliana</i> root gravitropism control protein (PIN2) gene, complete cds
10072	22597	35562	0.53	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10072	22597	35563	0.53	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10115	22610		0.72	2.0E-01	X78388.1	NT	<i>D.melanogaster</i> DNA mobile element (hoppe)
10304	22798	35799	0.88	2.0E-01	X97121.1	NT	<i>R.norvegicus</i> mRNA for NTR2 receptor
10720	23248	36293	2.77	2.0E-01	D89088.1	NT	<i>Salvelinus pluvius</i> mRNA for transferrin, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10720	23248	36284	2.77	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds
12162	24402		1.34	2.0E-01	AF206837.2	NT	Pinethales promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
12374	24887		1.95	2.0E-01	AF302773.1	NT	Homo sapiens ninein-Lm isoform (ninein) mRNA, complete cds
12386	24807	30788	2.81	2.0E-01	AW975297.1	EST_HUMAN	EST387405 MAGE resequences, MAGN Homo sapiens cDNA
12425	24610	30888	3.97	2.0E-01	A023592.1	EST_HUMAN	ov60a10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643610 3'
12449	24584		17.06	2.0E-01	AF078164.2	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds
115	12786		6.22	1.9E-01	7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Ahr1), mRNA
374	13023	25509	5.4	1.9E-01	AF004353.1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
684	13308	25792	1.47	1.9E-01	U32581.2	NT	Homo sapiens lambda/ota protein kinase C-interacting protein mRNA, complete cds
684	13308	25793	1.47	1.9E-01	U32581.2	NT	Homo sapiens lambda/ota protein kinase C-interacting protein mRNA, complete cds
691	13315	25800	6.6	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251189-011-d01 BT0502 Homo sapiens cDNA
692	13315	25800	6.82	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251189-011-d01 BT0502 Homo sapiens cDNA
1023	13633		1.92	1.9E-01	7305180	NT	Mus musculus interleukin 2 receptor, gamma chain (Il2rg), mRNA
1143	13746	26256	10.04	1.9E-01	AA358813.1	EST_HUMAN	EST167784 Fetal lung II Homo sapiens cDNA 5' end
1413	14006	26534	2.41	1.9E-01	AF061282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1482	14075		4.02	1.9E-01	AF184623.1	NT	Plasmodium vivax reticulocyte binding protein-2 (rbp-2) gene, complete cds
2185	14761	27331	1.29	1.9E-01	AA916492.1	EST_HUMAN	cl44h09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1528369 3' similar to gb:A03911
2422	14890	27563	3.27	1.9E-01	8922533	NT	GLIA DERIVED NEXIN PRECURSOR (HUMAN);
2949	15565	28039	4.1	1.9E-01	U66086.1	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA
2965	15580		6.58	1.9E-01	J00922.1	NT	Sigmoidon hispidus p53 gene, partial cds
3033	15649	28128	1.05	1.9E-01	U25148.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
3442	16050	28528	4.18	1.9E-01	D13197.1	NT	Rattus norvegicus brush border myosin-I (BBMI) mRNA, partial cds
3328	16131	28611	5.24	1.9E-01	R16487.1	EST_HUMAN	Mouse gene for immunoglobulin diversity region D1
3877	16475	28939	0.76	1.9E-01	AF264017.1	NT	yf42f10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129547 5'
4064	16681	29123	3.85	1.9E-01	AB006784.1	NT	Rattus norvegicus arylacetamide deacetylase gene, complete cds
4157	16749	29202	1.86	1.9E-01	AW754106.1	EST_HUMAN	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds
4315	16901	29345	1.17	1.9E-01	BE834943.1	EST_HUMAN	CM3-CT0315-271199-045-b11 CT0315 Homo sapiens cDNA
4688	17151	29597	0.69	1.9E-01	AL161493.2	NT	MR1-FN0010-290700-007-d04 FN0010 Homo sapiens cDNA
5156	17726		1.11	1.9E-01	AF223642.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 5
						NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
						EST_HUMAN	x29a07.x1 NCL_CGAP_U01 Homo sapiens cDNA clone IMAGE:2619444 3' similar to gb:M73779 RETINOIC
5789	18414		5.46	1.9E-01	AW130149.1	EST_HUMAN	ACID RECEPTOR ALPHA-1 (HUMAN);
5826	18450	31173	7.81	1.9E-01	AF127937.1	NT	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
6005	18625	31360	0.73	1.9E-01	AF091216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6046	18665		2.52	1.9E-01	AU133116.1	EST_HUMAN	AU133116 NT2RP4 Homo sapiens cDNA clone NT2RP4001328 5'
6469	18070	31855	1.07	1.9E-01	A1762391.1	EST_HUMAN	w154h02.x1 NCL_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2394099 3'
6523	19123	31915	1.23	1.9E-01	AW148452.1	EST_HUMAN	x14c08.x1 NCL_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2618030 3' similar to gb:X03559 ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);
7050	18069	30480	1.37	1.9E-01	R43212.1	EST_HUMAN	y009a12.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31663 3' similar to contains MER13 repetitive element;
7072	19644	32481	0.91	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7072	19644	32482	0.91	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7503	20025	32889	1.3	1.9E-01	U80922.1	NT	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPP8) gene, complete cds
7543	20063	32937	2.89	1.9E-01	AF072724.1	NT	Zea mays starch branching enzyme 1 (sbe1) gene, complete cds
7927	20469	33378	1.71	1.9E-01	AL161557.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
8620	21159	34074	12.12	1.9E-01	AB033024.1	NT	Homo sapiens mRNA for KIAA1198 protein, partial cds
8875	21414	34337	1.36	1.9E-01	M14588.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
8875	21414	34338	1.36	1.9E-01	M14588.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
8789	22287	35271	0.72	1.9E-01	AA912486.1	EST_HUMAN	cb96g10.s1 NCL_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537508 3' similar to contains Alu repetitive element
10140	22635	35626	0.71	1.9E-01	BE630353.1	EST_HUMAN	RC5-ET0082-060700-022-A02 ET0082 Homo sapiens cDNA
10140	22635	35627	0.71	1.9E-01	BE630353.1	EST_HUMAN	RC5-ET0082-060700-022-A02 ET0082 Homo sapiens cDNA
10523	23061	36071	2.02	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10523	23061	36072	2.02	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10635	23167	36178	2.06	1.9E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11377	23829	36891	1.88	1.9E-01	M22253.1	NT	Rattus norvegicus sodium channel I mRNA, complete cds
11571	24018	37088	2.69	1.9E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
12207	24431		1.33	1.9E-01	AF059900.1	NT	Drosophila melanogaster clathrin light chain mRNA, complete cds
12582	24874		3.69	1.9E-01	AF001168.1	NT	Arabidopsis thaliana receptor-like kinase LECRK1 (LECRK1) gene, complete cds
34	12713	25172	2.56	1.8E-01	U73200.1	NT	Mus musculus p116Rip mRNA, complete cds
281	15412	25423	1.87	1.8E-01	AB022090.1	NT	Mus musculus Cctg gene for chaperonin containing TCP-1 gamma subunit, partial cds
393	13039	25530	1.76	1.8E-01	4502532	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
778	13395	25896	0.77	1.8E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
1018	13628	26141	0.78	1.8E-01	AB192212.1	EST_HUMAN	w071f02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
1130	13732	26242	1.28	1.8E-01	AF000580.1	NT	Dictyostellium discoideum plasmid Ddp5, complete genome
1332	13926	26447	6.97	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1551	14143	26676	1.31	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1551	14143	26677	1.31	1.8E-01	6753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1887	14472		2.79	1.8E-01	4505036	NT	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA
1907	14492		2.22	1.8E-01	AT733708.1	EST_HUMAN	gq22d10.x5 NCI CGAP_Ki68 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:O75936 O75936 GAMMA BUTYROBETAINE HYDROXYLASE;
1958	14542	27098	1.52	1.8E-01	AB051897.1	NT	Mus musculus Scya8, Scya8, Scya16-ps, Scya5 genes for small inducible cytokine A8 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
2718	15273		2.28	1.8E-01	AW835728.1	EST_HUMAN	QV3-D70019-081299-038-g04 DT0018 Homo sapiens cDNA
2923	15540		2.36	1.8E-01	AF184589.1	NT	Jonopsidium acaule LEAFY protein (LEAFY2) gene, partial cds
2928	15544	28020	1.18	1.8E-01	AW182300.1	EST_HUMAN	x41a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659756 3'
3158	15772	28239	1.31	1.8E-01	AW995178.1	EST_HUMAN	QV0-BN0041-070300-147-c04 BN0041 Homo sapiens cDNA
3413	16021	28501	0.71	1.8E-01	BF183682.1	EST_HUMAN	601B09723R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040621 3'
3683	16284	28752	0.79	1.8E-01	H03369.1	EST_HUMAN	y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
3683	16284	28753	0.79	1.8E-01	H03369.1	EST_HUMAN	y45e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
4333	16920	29362	0.78	1.8E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4426	17012		4.07	1.8E-01	D37854.1	NT	Bovine NB25 mRNA for MHC class II (BdLA-DQB), complete cds
4654	17238	29681	6.59	1.8E-01	AL161556.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56
4886	17461	29914	2.51	1.8E-01	AB051897.1	NT	Mus musculus Scya8, Scya8, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
4928	17503	29950	1.03	1.8E-01	X92179.1	NT	S.tuberosum mRNA for alcohol dehydrogenase
5198	17763	30188	2.18	1.8E-01	AW814270.1	EST_HUMAN	MR3-ST0203-151289-112-g06 ST0203 Homo sapiens cDNA
5216	17781	30200	1.59	1.8E-01	AJ792382.1	EST_HUMAN	an28q07.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700028 5'
5257	17820	30245	1.5	1.8E-01	AF181258.1	NT	Mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds
5281	17843	30270	1.07	1.8E-01	A439881.1	EST_HUMAN	t57e04.x1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134590 3'
5288	17850	30276	0.59	1.8E-01	AF132115.1	NT	Arabidopsis thaliana cytochrome b-561 (CYTB561) gene, partial cds
5338	17899	30314	0.78	1.8E-01	AJ132844.1	NT	Broad bean wilt virus 2 genes encoding 119kDa protein, 104kDa protein, large coat protein, small coat protein
5338	17899	30315	0.78	1.8E-01	AJ132844.1	NT	Broad bean wilt virus 2 genes encoding 119kDa protein, 104kDa protein, large coat protein, small coat protein
5398	17956	30367	2.04	1.8E-01	AW809402.1	EST_HUMAN	MR4-ST0121-041199-019-b01 ST0121 Homo sapiens cDNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5976	18596	31331	1	1.8E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
6082	18699	31446	1.01	1.8E-01	N28629.1	EST_HUMAN	yc38h08.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:264063 5'
6277	18895	31653	1.1	1.8E-01	6678428	NT	Mus musculus Tnf receptor-associated factor 6 (Traf6), mRNA
6277	18885	31654	1.1	1.8E-01	6678428	NT	Mus musculus Tnf receptor-associated factor 6 (Traf6), mRNA
6635	19231	32035	2.03	1.8E-01	Q9QY14	SWISSPROT	FORHEAD BOX PROTEIN E3
6675	19271		2.24	1.8E-01	N94853.1	EST_HUMAN	Y62h02.r1 Soares_multiple_sclerosis_2NBHMSP Homo sapiens cDNA clone IMAGE:278163 5'
7077	19649	32487	1.22	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
7077	19649	32488	1.22	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
7117	19457	32272	0.71	1.8E-01	BE061353.1	EST_HUMAN	601648361R2 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:3932247 3'
8547	21086	34009	0.47	1.8E-01	AW966118.1	EST_HUMAN	EST378191 MAGE rescues, MAGI Homo sapiens cDNA
9268	21792	34741	1.13	1.8E-01	M73258.1	NT	Human cellular DNA/Human papillomavirus proviral DNA
9296	21896	34843	1.39	1.8E-01	9626232	NT	Bacteriophage like, complete genome
9412	21921		0.55	1.8E-01	AA493751.1	EST_HUMAN	nh02a05 s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943088 similar to contains L1.13 L1
9494	21894	34950	1.13	1.8E-01	P15272	SWISSPROT	repetitive element ;
9494	21894	34951	1.13	1.8E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
9532	22032	34990	0.95	1.8E-01	M26019.1	NT	S commune orotidine-5'-phosphate decarboxylase (URA1) gene, complete cds
9532	22032	34991	0.95	1.8E-01	M26019.1	NT	S commune orotidine-5'-phosphate decarboxylase (URA1) gene, complete cds
9694	22193	35166	0.62	1.8E-01	P08123	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9698	22197	35170	0.69	1.8E-01	U67548.1	NT	Methanococcus jannaschii section 90 of 150 of the complete genome
10039	22534		0.64	1.8E-01	AF200252.1	NT	Aquarius amplius cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial gene for mitochondrial product
10271	22766	35753	1.22	1.8E-01	X63440.1	NT	M.musculus mRNA for P19-protein tyrosine phosphatase
10516	23054	36066	2.37	1.8E-01	X77336.1	NT	A.thaliana mRNA for ribonucleotide reductase R2
10558	23094	36106	7.47	1.8E-01	U38906.1	NT	Bacteriophage r11 integrase, repressor protein (ro), dUTPase, holin and lysin genes, complete cds
10615	19649	32487	3.07	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
10615	19649	32488	3.07	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
10616	23148	36160	4.49	1.8E-01	AF019107.1	NT	Dicystotium discoidium unknown (DG1041) gene, complete cds
10897	23417	36434	1.84	1.8E-01	M59257.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 4
11337	23035	36045	4.3	1.8E-01	X57033.1	NT	B.taurus mRNA for potassium channel
11599	24042	37111	2.74	1.8E-01	8394421	NT	Rattus norvegicus Thromboxane receptor (Tbx2r), mRNA
11626	24068	37132	1.6	1.8E-01	U40487.1	NT	Mycobacterium smegmatis proton antiporter efflux pump (HrA), complete cds
11748	24146		2.04	1.8E-01	10086561	NT	Bovine ephemeral fever virus, complete genome

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11814	24186	31032	1.41	1.8E-01	BF348823.1	EST_HUMAN	602019928F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4155318 5'
12219	13926	26447	1.3	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1
12291	24491		5.61	1.8E-01	Q96682	SWISSPROT	DNA TERMINAL PROTEIN (BELLETT PROTEIN) (PTP PROTEIN)
12416	24569		23.47	1.8E-01	R24494.1	EST_HUMAN	YH48H10.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133027 5'
12459	24590		2.75	1.8E-01	Y11114.1	NT	E. dispar mRNA for hexokinase (hck1)
12502	25045	30507	1.58	1.8E-01	9506952	NT	Rattus norvegicus procollagen C-proteinase enhancer protein (Pcolee), mRNA
603	13232	25705	5.93	1.7E-01	BE385164.1	EST_HUMAN	601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3815768 5'
838	13454	25964	2.89	1.7E-01	X53330.1	NT	P dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
998	13608		8.63	1.7E-01	P35916	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
1096	13701	26210	0.67	1.7E-01	AF081810.1	NT	Lymantia disper nucleopolyhedrovirus, complete genome
1096	13701	26211	0.67	1.7E-01	AF081810.1	NT	Lymantia disper nucleopolyhedrovirus, complete genome
1853	14441	26898	0.95	1.7E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
2025	14607		2.84	1.7E-01	AF255051.1	NT	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product
2885	15503	27973	1.98	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2885	15503	27974	1.98	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2953	15569	28044	1.53	1.7E-01	AA336908.1	EST_HUMAN	EST41651 Endometrial tumor Homo sapiens cDNA 5' end
3027	15643	28121	1.9	1.7E-01	AJ238736.1	NT	Naja naja atra cbc-1 gene, exons 1-3
3027	15643	28122	1.9	1.7E-01	AJ238736.1	NT	Naja naja atra cbc-1 gene, exons 1-3
3139	15753	28220	1.91	1.7E-01	AF081514.1	NT	Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3412	16020	28500	1.11	1.7E-01	N55763.1	EST_HUMAN	J2346F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2346 5'
3494	16099	28574	1.26	1.7E-01	AJ268505.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
4012	16610	29083	4.99	1.7E-01	AJ235377.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/TEL gene
4658	17240		1.63	1.7E-01	X52936.1	NT	Schistosoma graxaria alpha repetitive DNA
4877	17452	29804	0.84	1.7E-01	AF217480.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
4965	17539	29981	1.07	1.7E-01	AJ247635.1	EST_HUMAN	qh57e09.x1 Soares fetal liver spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains ORF b1 ORF repetitive element;
5210	17775		0.88	1.7E-01	U28376.1	NT	Zea mays calcium-dependent protein kinase (MZECPK2) mRNA, complete cds
5242	17806	30227	1.02	1.7E-01	BF689719.1	EST_HUMAN	602196630F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4286646 5'

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5297	17859		1.08	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme 1b (ae) gene, complete cds
5342	17903	30319	0.6	1.7E-01	BF030010.1	EST_HUMAN	601557256F1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3827187 5'
5421	17978	30386	7.82	1.7E-01	J04479.1	NT	S.pneumoniae DNA polymerase I (pda) gene, complete cds
5604	18233	30683	1.92	1.7E-01	AA470686.1	EST_HUMAN	ne13a02.s1 NCL CGAP_C63 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5604	18233	30684	1.92	1.7E-01	AA470686.1	EST_HUMAN	ne13a02.s1 NCL CGAP_C63 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5779	18404	31120	0.7	1.7E-01	U43599.1	NT	Brugia pahangi microfilarial sheath protein SHP3 (shp3) gene, complete cds
6471	18072	31856	20.9	1.7E-01	H72118.1	EST_HUMAN	ys02g06.s1 Soares fetal liver spleen INFILS Homo sapiens cDNA clone IMAGE:213658 3'
6522	19122	31913	1.33	1.7E-01	AI370976.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6522	19122	31914	1.33	1.7E-01	AI370976.1	EST_HUMAN	ta29c11.x1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6937	18045	30467	0.71	1.7E-01	BE300286.1	EST_HUMAN	600944067T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960248 3'
6960	19537		2.26	1.7E-01	AF026552.3	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds
7074	19646		0.67	1.7E-01	Z92910.1	NT	Homo sapiens HFE gene
7272	19800	32657	2.83	1.7E-01	AP000422.1	NT	Escherichia coli O157:H7 genomic DNA, Sakai-VT2 prophage inserted region
7339	19668	32730	8.82	1.7E-01	BE734179.1	EST_HUMAN	601569022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843964 5'
7494	20017	32882	1.16	1.7E-01	P16724	SWISSPROT	PROBABLE PROCESSING AND TRANSPORT PROTEIN UL58 (HFLF0 PROTEIN)
7508	24784	32893	0.73	1.7E-01	Q01955	SWISSPROT	COLLAGEN ALPHA 3(IV) CHAIN PRECURSOR
7802	20345	33253	1.26	1.7E-01	AF000573.1	NT	Homo sapiens homotetrasial 1,2-dioxygenase gene, complete cds
7804	20448	33352	0.54	1.7E-01	AF150669.1	NT	Pseudomonas putida long-chain-fatty-acid-CoA ligase (lcaD) gene, complete cds
8219	20760	33674	6.62	1.7E-01	7706426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8219	20760	33675	6.62	1.7E-01	7706426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8631	21170	34087	0.58	1.7E-01	AW92873.1	EST_HUMAN	RC2.BN0032.120200-011-a10 BN0032 Homo sapiens cDNA
8662	21201	34119	3.28	1.7E-01	D00384.1	NT	Rat (SHR strain) SX1 gene
8778	21317	34239	0.68	1.7E-01	AF217413.1	NT	Homo sapiens neuriligin 3 isoform gene, complete cds, alternatively spliced
8778	21317	34240	0.68	1.7E-01	AF217413.1	NT	Homo sapiens neuriligin 3 isoform gene, complete cds, alternatively spliced
9095	21631	34569	0.46	1.7E-01	BE253142.1	EST_HUMAN	601116872F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'
9095	21631	34570	0.46	1.7E-01	BE253142.1	EST_HUMAN	601116872F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'
9509	22009	34967	7.72	1.7E-01	AP001508.1	NT	Bacillus halodurans genomic DNA, section 2/14
9614	22114	35077	0.56	1.7E-01	AW977455.1	EST_HUMAN	EST388564 MAGe resequences, MAGO Homo sapiens cDNA
9614	22114	35078	0.56	1.7E-01	AW977455.1	EST_HUMAN	EST388564 MAGe resequences, MAGO Homo sapiens cDNA
9631	22131	35096	2.47	1.7E-01	U19288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
9704	22203	35174	1.27	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (B7.05) env gene (partial)
9704	22203	35175	1.27	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (B7.05) env gene (partial)

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9722	22220	35195	0.81	1.7E-01	AJ251749.1	NT	Drosophila melanogaster mRNA for serine protease inhibitor (serpin-6), (sp8 gene)
10132	22627		2.24	1.7E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
10293	22787	35777	0.99	1.7E-01	11427203	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 2 (SLC7A2), mRNA
10295	22789	35779	1.72	1.7E-01	AA627972.1	EST_HUMAN	nc60e07 s1 NCI_CGAP_Co6 Homo sapiens cDNA clone IMAGE:1148292 3' similar to gb.L25081
10560	23096	36109	9.23	1.7E-01	BE390835.1	EST_HUMAN	TRANSFORMING PROTEIN RHOC (HUMAN);
10685	23215	36227	2.63	1.7E-01	AA814617.1	EST_HUMAN	601286547F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613258 5'
10991	23505	36536	8.7	1.7E-01	7106300	NT	6043a03 s1 NCI_CGAP_CNS1 Homo sapiens cDNA clone IMAGE:1426924 3'
10991	23505	36537	8.7	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
11558	24006		2.18	1.7E-01	P15272	SWISSPROT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
11643	24604		1.45	1.7E-01	AJ272584.1	NT	AMP NUCLEOSIDASE
11847	24079	37143	4.09	1.7E-01	11418157	NT	Blotbella aurantiaca mitochondrial partial COII gene for cytochrome c oxidase subunit II
11782	25004		1.94	1.7E-01	AL163278.2	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
12333	24517		1.38	1.7E-01	N40825.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
12381	24548	30905	12.95	1.7E-01	U01317.1	NT	yw82c12.r1 Soares_placenta_8to9weeks_2NbHP809W Homo sapiens cDNA clone IMAGE:258742 5'
12609	24693		1.33	1.7E-01	AJ132510.1	NT	Human beta globin region on chromosome 11
131	12798	25285	1.57	1.6E-01	AF217532.1	NT	Sus scrofa c-fos gene, exons 1-4
706	15398	25816	1.56	1.6E-01	R31497.1	EST_HUMAN	Homo sapiens mevalonate kinase gene, exon 6 and 7
1569	14181	26692	4.35	1.6E-01	AF298117.1	NT	yh75f12.r1 Soares_placenta_Nb2HP Homo sapiens cDNA clone IMAGE:135599 5'
1968	14552	27108	2.8	1.6E-01	P22063	SWISSPROT	Homo sapiens homeobox protein OTX2 gene, complete cds
2028	14610		1.08	1.6E-01	U10334.1	NT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
2427	15466	27569	0.96	1.6E-01	X94232.1	NT	Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds
2535	15099	27672	1.12	1.6E-01	AB037729.1	NT	H.sapiens mRNA for novel T-cell activation protein
2917	15534	28006	11.95	1.6E-01	AF185589.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2917	15534	28007	11.95	1.6E-01	AF185589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3041	16657	28137	1.17	1.6E-01	AE001862.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3695	16296	28765	1.35	1.6E-01	AJ003165.1	NT	Dainococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
3695	16296	28766	1.35	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3840	16439	28901	0.71	1.6E-01	AE000962.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
4072	16668		2.65	1.6E-01	AE004413.1	NT	Archaeoglobus fulgidus section 145 of 172 of the complete genome
4422	17007	28450	11.02	1.6E-01	AF176680.1	NT	Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome
4554	17137		3.42	1.6E-01	AW968601.1	EST_HUMAN	Homo sapiens apelin gene, complete cds
							EST380677 MAGC resequences, MAGJ Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4563	17146		4.68	1.6E-01	6753319	NT	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA
5057	17630	30074	0.84	1.6E-01	P40631	SWISSPROT	MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) [CONTAINS: LINKER HISTONE PROTEINS ALPHA, BETA, DELTA AND GAMMA]
5080	17653	30093	1.45	1.6E-01	AA098343.1	EST_HUMAN	284409.s1 Strategene colon (#937204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR:E221855
5101	17673	30112	1.26	1.6E-01	AJ006356.1	NT	E221855 38,855 BP SEGMENT OF CHROMOSOME XIV.;
5101	17673	30113	1.26	1.6E-01	AJ006356.1	NT	Lycopodium esculentum RsaI fragment 2, satellite region
5358	17818		1.81	1.6E-01	BF208302.1	EST_HUMAN	Lycopodium esculentum RsaI fragment 2, satellite region
5359	17919	30333	1.23	1.6E-01	A1874074.1	EST_HUMAN	601872523F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4096885 5'
5587	18218	30668	0.76	1.6E-01	L40608.1	NT	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5713	18339	30844	2.76	1.6E-01	AW197496.1	EST_HUMAN	xm43101.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2686969 3' similar to TR:O75984 O75984 HYPOTHETICAL 127.6 KD PROTEIN;
5713	18339	30845	2.76	1.6E-01	AW197496.1	EST_HUMAN	xm43101.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2686969 3' similar to TR:O75984 O75984
5725	18351	31054	2.12	1.6E-01	AF034716.1	NT	HYPOTHETICAL 127.6 KD PROTEIN;
6179	18789	31558	0.84	1.6E-01	BE925803.1	EST_HUMAN	Rattus norvegicus CCAAT/enhancer binding protein epsilon (cebpe) gene, complete cds
6559	19157	31953	2	1.6E-01	AL161588.2	NT	RC3-BN0034-310800-113-h01 BN0034 Homo sapiens cDNA
6559	19157	31954	2	1.6E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7043	18063	30453	3.49	1.6E-01	AW291215.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7753	20261	33157	1.44	1.6E-01	AW246359.1	EST_HUMAN	U1-H-B12-epi-b-06-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3'
7770	20278		0.75	1.6E-01	AU136525.1	EST_HUMAN	2822248.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2622248 5'
7810	20353	33262	1.43	1.6E-01	L49349.1	NT	AU136525 PLACE1 Homo sapiens cDNA clone PLACE1004466 5'
7968	20510		0.55	1.6E-01	BE244087.1	EST_HUMAN	Gorilla gorilla androgen receptor gene, partial exon
8082	20604	33515	0.76	1.6E-01	U38243.1	NT	TCBAP1E0607 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0607
8567	21106	34025	0.77	1.6E-01	Z99119.1	NT	cDNA clone TCBAP0607
8760	21299	34220	0.65	1.6E-01	R13873.1	EST_HUMAN	Bacteroides vulgatus beta-lactamase (ctxA) gene, complete cds and mobilization protein (mobA) gene, complete cds
8863	21402		0.64	1.6E-01	L36861.1	NT	Bacillus subtilis complete genome (section 16 of 21); from 2697771 to 3213410
8901	21439	34362	1.91	1.6E-01	Z49501.1	NT	y60108.r1 Soares infant brain TNIB Homo sapiens cDNA clone IMAGE:26873 5'
9039	21576		0.8	1.6E-01	AF111167.2	NT	Homo sapiens guanylate cyclase activating protein (GCAP) gene exons 1-4, complete cds
9569	22069		1.93	1.6E-01	BF375171.1	EST_HUMAN	S. cerevisiae chromosome X reading frame ORF YJR001w
9572	22072	35033	1.86	1.6E-01	Z49501.1	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
							RC3-ST0200-041199-011-h01 ST0200 Homo sapiens cDNA
							S. cerevisiae chromosome X reading frame ORF YJR001w

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9607	22107		1.06	1.6E-01	BE155964.1	EST_HUMAN	PM2-HT0353-270100-004-f11 HT0353 Homo sapiens cDNA
10536	23073	36087	2.7	1.6E-01	AW850853.1	EST_HUMAN	IL3-CT0220-111199-028-G01 CT0220 Homo sapiens cDNA
10860	23401	36418	1.55	1.6E-01	BE259849.1	EST_HUMAN	60T145793F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3161183 5'
10984	23508		8.03	1.6E-01	AF108064.1	NT	Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds
11289	23741	36798	10.88	1.6E-01	6671552	NT	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Aptb1), mRNA
11660	25019		1.72	1.6E-01	6679466	NT	Mus musculus protein kinase, cGMP-dependent, type II (Prkg2), mRNA
11784	24169	36778	5.34	1.6E-01	AV719585.1	EST_HUMAN	AV719585 GLC Homo sapiens cDNA clone GLCEMF07 5'
12095	24362	30968	1.55	1.6E-01	L14833.1	NT	Rat convertase PCS mRNA, 5' end
12128	24382		1.75	1.6E-01	AW839711.1	EST_HUMAN	RC1-LT0074-120200-014-h01_1 LT0074 Homo sapiens cDNA
12229	24821		11.74	1.6E-01	AB045310.1	NT	Cucumis sativus KS mRNA for ent-kaurane synthase, complete cds
12407	24564		5.11	1.6E-01	AK024496.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds
12497	24625		3.96	1.6E-01	AF287344.1	NT	Fuchsia hybrid cultivar Qiu 94208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
12521	24637	30898	1.88	1.6E-01	9506522	NT	Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Capp5), mRNA
269	12926	25412	1.76	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
269	12926	25413	1.76	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
613	15387		2.16	1.5E-01	AV711696.1	EST_HUMAN	AV711696 DCA Homo sapiens cDNA clone DCAADH06 5'
815	13433	25938	1.04	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1131	13734	26244	0.84	1.5E-01	AJ009735.1	NT	Cyprinus carpio mRNA for EGG522 myosin heavy chain, 3'UTR
1136	13739	26248	2.28	1.5E-01	AJ251885.1	NT	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1
1152	13755		1.61	1.5E-01	L38125.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1258	13855	26371	0.79	1.5E-01	AW195516.1	EST_HUMAN	xn39d11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2696085 3'
1318	13912	26432	3.12	1.5E-01	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1318	13912	26433	3.12	1.5E-01	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1529	14121	26660	1.84	1.5E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
1951	14535	27091	1.62	1.5E-01	AW444451.1	EST_HUMAN	UIH-B13-akb-b-09-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733641 3'
2736	15291	27859	1.17	1.5E-01	BF695381.1	EST_HUMAN	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247637 5'
2938	15554		1.01	1.5E-01	AW572516.1	EST_HUMAN	xw56a02.x2 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:4247637 5'
3070	15685	28157	0.62	1.5E-01	M61441.1	NT	THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN); Bos taurus factor V variant 2 (factor V) mRNA, complete cds
3395	16003	28484	6.87	1.5E-01	AA935049.1	EST_HUMAN	cc88d05.s1 NCI_CGAP_GCA Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:M11433
3415	16023	28504	0.65	1.5E-01	Z23104.1	NT	RETINOL-BINDING PROTEIN 1, CELLULAR (HUMAN); L. stagnalis mRNA for G protein-coupled receptor
3415	16023	28505	0.65	1.5E-01	Z23104.1	NT	L. stagnalis mRNA for G protein-coupled receptor

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3474	16080	28553	0.99	1.5E-01	AW612237.1	EST_HUMAN	hh29f02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2956539 3' similar to contains element MER16 repetitive element;
3819	18419	28881	2.13	1.5E-01	U09964.1	NT	Mus musculus (CR/Swiss glyceroldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3835	18434	28896	0.94	1.5E-01	7108358	NT	XYNA; Thermoanaerobacterium; xynA; 4182 base-pairs
3849	18447	28908	0.58	1.5E-01	M97882.1	NT	h10f06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2981411 3'
3934	16532	28999	2.74	1.5E-01	AW685983.1	EST_HUMAN	Populus trichocarpa cv. Trichobal ABI3 gene
3951	16549	29017	0.9	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobal ABI3 gene
3951	16549	29018	0.9	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobal ABI3 gene
4124	18717	29173	0.82	1.5E-01	AW368659.1	EST_HUMAN	RC2-HT0149-191099-012-c09 HT0149 Homo sapiens cDNA
4262	16848	29296	9.82	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4833	17411	29884	1.29	1.5E-01	BF087685.1	EST_HUMAN	602067182F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4066223 5'
4863	15291	27859	2.03	1.5E-01	BF695381.1	EST_HUMAN	602083289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
4908	17481	28938	0.92	1.5E-01	BE173798.1	EST_HUMAN	CNO-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
4908	17481	28939	0.92	1.5E-01	BE173798.1	EST_HUMAN	CNO-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
5139	17711	30141	1.59	1.5E-01	AL181590.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
5481	18088	30414	1.96	1.5E-01	P07996	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5489	18123	30530	0.8	1.5E-01	AF256652.1	NT	Callinectes mercedis MHC class II beta chain (hclbeta) gene, complete cds
5531	18163		5.6	1.5E-01	P15196	SWISSPROT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN)
5729	18355	31059	4.68	1.5E-01	AW850754.1	EST_HUMAN	IL3-CT0219-180200-064-F10 CT0219 Homo sapiens cDNA
5787	18393	31106	6.97	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGfa) mRNA, complete cds
5787	18393	31107	6.97	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGfa) mRNA, complete cds
6156	18789	31532	1.4	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
6156	18789	31533	1.4	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
6194	18804	31573	1.96	1.5E-01	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
6342	18948	31725	3.23	1.5E-01	BE27658.1	EST_HUMAN	801564322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833981 5'
6394	18987		1.86	1.5E-01	4508396	NT	Homo sapiens RAD54 (S.cerevisiae)-like (RAD54L) mRNA
6484	19085	31887	1.75	1.5E-01	AF134907.1	NT	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
6626	24765	32027	1.94	1.5E-01	AE001039.1	NT	Archaeoglobus fulgidus section 68 of 172 of the complete genome
6652	19248	32050	4.63	1.5E-01	11417298	NT	Homo sapiens chromosome 5 open reading frame 3 (C5ORF3), mRNA

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6663	19259	32063	1.5	1.5E-01	P48508	SWISSPROT	GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
6702	19297	32101	2.16	1.5E-01	Q28462	SWISSPROT	AMELOGENIN
6786	19377	32192	0.95	1.5E-01	AA714780.1	EST_HUMAN	nm30d10.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241971 3'
6813	19404	32220	1.59	1.5E-01	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF8)
7055	18074	30464	6.39	1.5E-01	AW970295.1	EST_HUMAN	EST382378 IMAGE sequences, MAGK Homo sapiens cDNA
7268	19796		1.9	1.5E-01	AF210842.1	NT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
7423	19847	32813	1.5	1.5E-01	A1973157.1	EST_HUMAN	wr52c08.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3'
7589	20104	32979	1.02	1.5E-01	AF299073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7589	20104	32980	1.02	1.5E-01	AF299073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7596	20110	32984	1.71	1.5E-01	AW500611.1	EST_HUMAN	UI-HF-BN0-akk-d-05-Q-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
7596	20110	32985	1.71	1.5E-01	AW500611.1	EST_HUMAN	UI-HF-BN0-akk-d-05-Q-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
7722	20230	33119	0.71	1.5E-01	U46960.1	NT	Saccharomyces cerevisiae weak multicopy suppressor of lost-1 (SOL3) gene, complete cds
8002	20544	33446	1.1	1.5E-01	P21303	SWISSPROT	MEROZOITE RECEPTOR PK66 PRECURSOR (66 KD PROTECTIVE MINOR SURFACE ANTIGEN)
8161	20702	33617	0.95	1.5E-01	AA970317.1	EST_HUMAN	od55g12.s1 NCI_CGAP_K1d5 Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb:M26062
8254	20795		1.11	1.5E-01	BE884799.1	EST_HUMAN	INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
8339	20880		11.5	1.5E-01	C16800.1	EST_HUMAN	601510523F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912004 5'
8372	20912	33832	1.82	1.5E-01	L27835.1	NT	C16800 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-529H09 5'
8529	21068	33987	2.04	1.5E-01	D84478.1	NT	P angasiadon gigas growth hormone (GH) mRNA, complete cds
8550	21089		0.86	1.5E-01	P43446	SWISSPROT	Homo sapiens mRNA for ASK1, complete cds
8772	21311	34234	1.23	1.5E-01	4501972	NT	WNT-10A PROTEIN PRECURSOR
9033	21570	34499	2.46	1.5E-01	N74226.1	EST_HUMAN	Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA
9121	21657	34598	1.06	1.5E-01	BF585465.1	EST_HUMAN	za59e06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:298866 3' similar to PIR:S44443 S44443 RAD23 protein homolog2 - human ;
9128	21663		2.63	1.5E-01	AV754819.1	EST_HUMAN	GVO000404 Human Psoriasis Differential Display Homo sapiens cDNA
9326	21840		0.94	1.5E-01	AU130007.1	EST_HUMAN	AV754819 TP Homo sapiens cDNA clone TPAAHB12 5'
9374	20313	33215	7.21	1.5E-01	U00455.1	NT	AU130007 NT2RP3 Homo sapiens cDNA clone NT2RP3000080 5'
9731	22229	35206	0.48	1.5E-01	M77144.1	NT	Acipenser transmontanus vitellogenin mRNA, partial cds
9835	22333	35314	8.51	1.5E-01	AF007570.1	NT	Human type II 3-beta hydroxysteroid dehydrogenase/ 5-delta - 4-delta isomerase gene, complete cds
9835	22333	35315	8.51	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10104	22569	35591	2.54	1.5E-01	X98852.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10188	22863		3.34	1.5E-01	AB027759.1	NT	P. lentusculi mRNA for integrin beta subunit
						NT	Mesocricetus auratus mRNA for collagen type XVII, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10210	22705	35698	2.82	1.5E-01	AI814046.1	EST_HUMAN	wk53h12.x1 NCI CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10210	22705	35699	2.82	1.5E-01	AI814046.1	EST_HUMAN	wk53h12.x1 NCI CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10288	22783	35775	1.75	1.5E-01	U40932.1	NT	Danio rerio transcription factor Pax8b (Pax8) mRNA, complete cds
10433	22927	35933	1.97	1.5E-01	AJ011964.1	NT	Claviceps purpurea ps1 gene
10433	22927	35934	1.97	1.5E-01	AJ011964.1	NT	Claviceps purpurea ps1 gene
10704	23233	36245	5.45	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
10704	23233	36246	5.45	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
10854	23469	36494	1.71	1.5E-01	AW841915.1	EST_HUMAN	IL5-CN0024-030300-025-D04 CN0024 Homo sapiens cDNA
11045	18947	32813	2.44	1.5E-01	AI973157.1	EST_HUMAN	wfs2c08.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3'
11739	24875		79.5	1.5E-01	BF700582.1	EST_HUMAN	802128753F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285549 5'
12125	24381		1.43	1.5E-01	AF030358.2	NT	Rattus norvegicus chemokine CX3C mRNA, complete cds
12190	24699		7.05	1.5E-01	R83077.1	EST_HUMAN	yp87e04.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:184430 5'
12288	24820		3.12	1.5E-01	AV741272.1	EST_HUMAN	AV741272 CB Homo sapiens cDNA clone CBDAGD04 5'
12406	24824	30794	16.12	1.5E-01	AL139074.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 1/8
12821	24699	30862	3	1.5E-01	Q8Z0Y8	SWISSPROT	VOL TAGE-DEPENDENT T-TYPE CALCIUM CHANNEL ALPHA-1I SUBUNIT (CAVT.3)
12832	24709	30865	11.33	1.5E-01	AJ276242.1	NT	Sus scrofa mRNA for sodium iodide symporter
321	12975		1.48	1.4E-01	AF009663.1	NT	Homo sapiens T cell receptor beta locus, TCRBV85P to TCRBV21S2A2 region
943	13556		2.71	1.4E-01	D78638.1	NT	Xenopus laevis mRNA for DNA (cytosine-5-)methyltransferase, complete cds
1302	13998		1.59	1.4E-01	T91864.1	EST_HUMAN	yd54c01.s1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:112032 3'
1784	14374		1.35	1.4E-01	6679980	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1787	14377	26921	1.39	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
2029	14611		10.08	1.4E-01	AA720615.1	EST_HUMAN	ny72d07.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283821 3'
2514	15078	27650	1.4	1.4E-01	P30706	SWISSPROT	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
2818	15370	27940	4.1	1.4E-01	AI933496.1	EST_HUMAN	wm74d01.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2441865 3'
4253	16841	29290	10.32	1.4E-01	AI699094.1	EST_HUMAN	b56c02.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4253	16841	29291	10.32	1.4E-01	AI699094.1	EST_HUMAN	b56c02.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4321	16807	29349	3.71	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
							z50d001.s1 Soares_fetal_liver_spleen_1NFS_S1 Homo sapiens cDNA clone IMAGE:453873 3' similar to gb:X01057_mn1 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN); contains Alu repetitive element;
4501	17085		0.61	1.4E-01	AA776287.1	EST_HUMAN	Homo sapiens phosphodiesterase 4A, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E2) (PDE4A), mRNA
4784	17364	29815	0.59	1.4E-01	5453861	NT	

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5329	17890		1.74	1.4E-01	BE910013.1	EST_HUMAN	601498056F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900157 5'
5509	18142	30554	4.49	1.4E-01	T90877.1	EST_HUMAN	ye13c11.s1 Striatogene lung (#937210) Homo sapiens cDNA clone IMAGE:117812 3'
5532	18164	30577	4.24	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5532	18164	30578	4.24	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
6440	19042	31830	2.7	1.4E-01	BE328891.1	EST_HUMAN	h87c02.x1 NCL_OGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133538 3'
6608	19205	32012	6.4	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6608	19205	32013	6.4	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6686	19282	32085	3.78	1.4E-01	AW082796.1	EST_HUMAN	xb71d12.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2581751 3'
6899	19285		1.53	1.4E-01	BE266536.1	EST_HUMAN	601193523F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537581 5'
6718	19312	32115	2.07	1.4E-01	BF378533.1	EST_HUMAN	QV1-UM0036-080300-103-009 UM0036 Homo sapiens cDNA
7180	19712		0.81	1.4E-01	AL118568.1	EST_HUMAN	DKFZp761A0910_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A0910 5'
7419	19943		1.83	1.4E-01	AW015373.1	EST_HUMAN	U1-H-B10-aat-c-09-0-U1.s1 NCL_OGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
7617	20130	33005	1.94	1.4E-01	U85945.1	NT	Oryctolagus cuniculus fructose 1,6-bisphosphate aldolase (AldB) gene, complete cds
7733	20241	33132	1.77	1.4E-01	A1305192.1	EST_HUMAN	ql90b12.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1879583 3'
8410	20950		1.28	1.4E-01	AV659047.1	EST_HUMAN	AV659047 GLC Homo sapiens cDNA clone GLCF3H08 3'
8719	21258		0.62	1.4E-01	A1436093.1	EST_HUMAN	h92b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126111 3' similar to TR:O02710 O02710 GAG POLYPROTEIN.
8844	21383	34308	4.58	1.4E-01	AA307073.1	EST_HUMAN	EST178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
8924	21462	34379	0.62	1.4E-01	AW023636.1	EST_HUMAN	df58b03.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487485 5'
9050	21587	34518	1.21	1.4E-01	R62746.1	EST_HUMAN	y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9050	21587	34519	1.21	1.4E-01	R62746.1	EST_HUMAN	y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9114	21650	34591	8.46	1.4E-01	BF310959.1	EST_HUMAN	601985465F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5'
9199	21716	34680	1.09	1.4E-01	W93411.1	EST_HUMAN	zd94a04.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains element KER repetitive element;
9280	21806	34757	1.47	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
9280	21806	34758	1.47	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
9371	20310	33213	1.95	1.4E-01	AF121361.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase la1 (IAL), and zinc finger protein (DNZ1) genes, complete cds
9898	22395	35371	1.18	1.4E-01	AF023813.1	NT	Macromitrium levatum small ribosomal protein 4 (rps4) gene, chloroplast gene encoding chloroplast protein, partial cds
10000	22495	35484	0.51	1.4E-01	AW021908.1	EST_HUMAN	df28h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10000	22495	35485	0.51	1.4E-01	AW021908.1	EST_HUMAN	df28h08.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10157	22652	35645	0.72	1.4E-01	BF375285.1	EST_HUMAN	MR3-ST0218-211289-013-a08 ST0218 Homo sapiens cDNA
10157	22652	35646	0.72	1.4E-01	BF375285.1	EST_HUMAN	MR3-ST0218-211289-013-a08 ST0218 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10360	22854		0.73	1.4E-01	T84233.1	EST_HUMAN	yd47d03.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:111365 5'
10469	22983	35991	0.7	1.4E-01	Z99117.1	NT	Bacillus subtilis complete genome (section 14 of 21); from 2599451 to 2812870
10587	23122		1.89	1.4E-01	AA811480.1	EST_HUMAN	cd99a03.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1320384 3'
10722	23250	36285	3.2	1.4E-01	R53400.1	EST_HUMAN	y70c06.r1 Soares breast2NBHst Homo sapiens cDNA clone IMAGE:154098 5'
10974	23489	36518	1.56	1.4E-01	P09648	SWISSPROT	INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT)(INTEGRIN ALPHA-F)(VLA-5)(CD49E)
11172	23678	36724	1.82	1.4E-01	X66092.1	NT	C.pertingens ORF for putative membrane transport protein
11210	19943		1.96	1.4E-01	AW015373.1	EST_HUMAN	U-H-B10-eat-c-09-Q-UJ.s1 NCL CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
11344	23042	36052	2.4	1.4E-01	U28760.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
12061	24344	30963	4.44	1.4E-01	X74773.1	NT	P. salina plastid gene secY
12074	24352		3.65	1.4E-01	11988117	NT	Rattus norvegicus desmth (Des), mRNA
12123	25082		1.52	1.4E-01	BES13802.1	EST_HUMAN	801315639F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634328 5'
12223	24444		9.33	1.4E-01	AF083221.1	NT	Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycylamide ribonucleotide transferase (GART) genes, complete cds
12235	24451		1.96	1.4E-01	D84004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002985
12315	25088		1.77	1.4E-01	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
12340	24522		2.01	1.4E-01	AA452305.1	EST_HUMAN	zx30e12.r1 Soares_total_tetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788014 5' similar to contains
12545	24900		3.55	1.4E-01	D82883.1	NT	Alu repetitive element
12627	24705		1.33	1.4E-01	AW377998.1	EST_HUMAN	Mus musculus mRNA for prolidase, complete cds
344	12998	25481	2.28	1.3E-01	4758487	NT	MRO-HT0208-221299-204-c08 HT0208 Homo sapiens cDNA
344	12998	25482	2.28	1.3E-01	4758487	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
555	13186	25664	3.25	1.3E-01	AB013139.1	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
684	13288	25769	3.03	1.3E-01	AJ277606.1	NT	Homo sapiens gene for NBS1, complete cds
684	13288	25770	3.03	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
877	13491	26009	0.78	1.3E-01	X63330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
927	13540	26058	1.44	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1064	13669	26179	1.36	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1168	13768		2.03	1.3E-01	AL115285.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1257	13854	26370	1.36	1.3E-01	AV712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAAF05 5'
1493	14085		0.97	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein CMS mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2002	14584	27143	2.32	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2215	14780		1.21	1.3E-01	AJ243578.1	NT	Rhodopseudomonas acidophila pucB5, pucA5, pucB6, pucA7, pucB8, pucA8 and pucC genes and ORF151
2329	14900		1.56	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-191099-032-d12 ST0173 Homo sapiens cDNA
2421	14989		3.74	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2622	15184	27750	1.55	1.3E-01	M86918.1	NT	Carassius auratus keratin type I mRNA, complete cds
3402	16011	28490	0.61	1.3E-01	AF196779.1	NT	Homo sapiens transcription factor IGDM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a2
3498	16103	28578	0.99	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
3785	16385	28850	1.19	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3785	16385	28851	1.19	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3791	16391	28856	0.8	1.3E-01	AB032159.1	NT	Homo sapiens DD4 gene for dihydrolipoyl transacylase 4 [AKR1C4], exon 2
3848	16385	28850	0.62	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3948	16385	28851	0.62	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7)
3875	16473	28937	0.74	1.3E-01	6978940	NT	Rattus norvegicus Fibrinogen, gamma polypeptide (Fgg), mRNA
4060	16657		1.3	1.3E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4125	13288	25769	1.65	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
4125	13288	25770	1.65	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
4218	16806		0.95	1.3E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome
4238	16826		4.04	1.3E-01	AW384341.1	EST_HUMAN	QV3-DT0018-081299-036-a03 DT0018 Homo sapiens cDNA
4246	16834	29285	2.25	1.3E-01	AF026803.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4265	16851	29299	21.7	1.3E-01	AW273741.1	EST_HUMAN	xv23f10.x1 Soares_NFL_T_CBC_S1 Homo sapiens cDNA clone IMAGE:2813995 3'
4404	16889		1.55	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4577	17160	29603	0.62	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolipoyl transacylase mRNA, complete cds
4831	17214	29685	2.35	1.3E-01	BE272339.1	EST_HUMAN	601128086F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:2990063 5'
4998	18009		0.94	1.3E-01	BE884017.1	EST_HUMAN	601510347F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3911987 5'
5056	17629	30073	1.05	1.3E-01	D76842.1	EST_HUMAN	HUM520C02B Human placenta polyA+ (TFJwara) Homo sapiens cDNA clone GEN-520C02 5'
5279	17841	30288	4.06	1.3E-01	A1432531.1	EST_HUMAN	th38c10.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2120562 3'
5396	17954	30365	0.65	1.3E-01	AP000005.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 994001-1166000 nt. position (5/7)

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5444	17999	30402	13.66	1.3E-01	AA991841.1	EST_HUMAN	$\alpha 45\alpha 07$.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1619748 3' similar to SW:YEY6_YEAST P40093 HYPOTHETICAL 38.2 KD PROTEIN IN BEM2-NCB1 INTERGENIC REGION. [1];
5444	17999	30403	13.66	1.3E-01	AA991841.1	EST_HUMAN	$\alpha 45\alpha 07$.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1619748 3' similar to SW:YEY6_YEAST P40093 HYPOTHETICAL 38.2 KD PROTEIN IN BEM2-NCB1 INTERGENIC REGION. [1];
5528	18160	30575	0.69	1.3E-01	AW466988.1	EST_HUMAN	ha07b06.x1 NCL_OGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872879 3' similar to contains L1b1 L1 L1 repetitive element;
5595	18196	30842	2.76	1.3E-01	AW804417.1	EST_HUMAN	QV0-UM0093-100400-188-a08 UM0093 Homo sapiens cDNA
5682	18318		0.76	1.3E-01	AF107783.1	NT	Emericella nidulans DNA-dependent RNA polymerase II RP8140 (RPB2) gene, partial cds
5772	18397		0.78	1.3E-01	AF056890.1	NT	Hepatitis C virus 68 CL10 genome polyprotein gene, partial cds
5899	18521	31246	0.89	1.3E-01	BF210820.1	EST_HUMAN	601874591F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101119 5'
6609	19206	32014	15.81	1.3E-01	AB031326.1	NT	Schistosoma haematobium gene for Alp41, complete cds
6684	19280	32083	2.07	1.3E-01	X68891.1	NT	Cjacchus intron 4 of visual pigment gene (red allele)
6883	19618		0.82	1.3E-01	W26367.1	EST_HUMAN	26f3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
7305	19833		1.94	1.3E-01	H48684.1	EST_HUMAN	Y33d02.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:207075 5'
7914	20442	33362	0.67	1.3E-01	BE272339.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2890063 5'
7945	20487	33397	0.69	1.3E-01	BF690522.1	EST_HUMAN	Homo sapiens PRO0611 protein (PRO0611), mRNA
8190	20721		0.47	1.3E-01	BE662528.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4296074 3'
8286	20827		4.61	1.3E-01	Z74102.1	NT	601335829F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3680934 5'
8325	20866		3.78	1.3E-01	8923918	NT	S cerevisiae chromosome IV reading frame ORF YDL054c
8485	21005	33923	1.05	1.3E-01	BF690522.1	EST_HUMAN	Homo sapiens core histone macroH2A.2 (MACROH2A2), mRNA
8878	21416	34339	0.52	1.3E-01	R11172.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4296074 3'
8878	21416	34340	0.52	1.3E-01	R11172.1	EST_HUMAN	Y39g11.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:129284 5' similar to SP:RL2B_RAT P29316 60S RIBOSOMAL PROTEIN ;
9148	21681	34625	1.64	1.3E-01	11068003	NT	Y39g11.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:129284 5' similar to SP:RL2B_RAT P29316 60S RIBOSOMAL PROTEIN ;
9148	21681	34626	1.64	1.3E-01	11068003	NT	Plutella xylostella granulovirus, complete genome
9393	21816	34766	5.08	1.3E-01	AF023129.1	NT	Plutella xylostella granulovirus, complete genome
9686	22185		0.8	1.3E-01	N86348.1	EST_HUMAN	Oryctolagus cuniculus H+K-A1Pase alpha 2c subunit mRNA, complete cds
9884	22459		0.8	1.3E-01	8393940	NT	J7837F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7837 5' similar to B-CELL RECEPTOR ASSOCIATED PROTEIN (BAP) 29
10036	22631	35526	0.83	1.3E-01	AW851599.1	EST_HUMAN	Rattus norvegicus peptidyl arginine deiminase, type IV (Pd4), mRNA
							MR2-CT0222-201089-001-e01 CT0222 Homo sapiens cDNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10282	24797	35776	0.9	1.3E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
10417	22911	35911	0.82	1.3E-01	AU121237.1	EST_HUMAN	AU121237 HEMBB1 Homo sapiens cDNA clone HEMBB1002387 5'
10511	23049		3.33	1.3E-01	BF330699.1	EST_HUMAN	MR4-B T0358-130700-010-h08 B T0358 Homo sapiens cDNA
10975	23490	36520	1.58	1.3E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
11130	23638		5.15	1.3E-01	6671745	NT	Mus musculus cofilin 2, muscle (Cif2), mRNA
11466	23918	36984	3.61	1.3E-01	BE279449.1	EST_HUMAN	601158052F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504804 5'
11902	24241	31007	1.64	1.3E-01	BE618346.1	EST_HUMAN	601462741F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3666003 5'
12048	24332		3.27	1.3E-01	AJ242790.1	NT	Gallus gallus scyc1 gene for lympholactin, exons 1-3
12466	24594		1.53	1.3E-01	AW001114.1	EST_HUMAN	wu24409.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520977 3' similar to
12647	24721		1.84	1.3E-01	BE598603.1	EST_HUMAN	TR:O60287 O60287 KIAA0539 PROTEIN. ;
406	13081	25573	10.81	1.2E-01	A1421744.1	EST_HUMAN	601844622R2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3929980 3'
449	12678		1.43	1.2E-01	U69912.1	NT	ANNNIN V (HUMAN);
573	13203		2.58	1.2E-01	AF039442.1	NT	Dicystostellum discoideum ORF DG1016 gene, partial cds
1419	14012	26541	2.31	1.2E-01	AU149146.1	EST_HUMAN	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1419	14012	26542	2.31	1.2E-01	AU149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1426	14019		3.26	1.2E-01	AV735249.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001691 3'
1431	14023		6.69	1.2E-01	AL445066.1	NT	AV735249 cDNA Homo sapiens cDNA clone cDNAJB11 5'
1554	14146		1.19	1.2E-01	AA897474.1	EST_HUMAN	Thermoplasma acidophilum complete genome; segment 4/5
1673	14265	26799	1.48	1.2E-01	Q14934	SWISSPROT	al48e09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TR:Q16671
1691	14283	26819	2.77	1.2E-01	A1285402.1	EST_HUMAN	Q16671 ANTI-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR. ;
1805	14395		21.02	1.2E-01	X89211.1	NT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR
1864	14548		2.23	1.2E-01	AF449368.1	EST_HUMAN	NFAT3) (NF-ATC4) (NF-AT3)
2226	14801	27373	1.31	1.2E-01	BF249490.1	EST_HUMAN	qf69f09.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1960553 3'
2325	14896	27470	1.08	1.2E-01	AL163213.2	EST_HUMAN	H sapiens DNA for endogenous retroviral like element
2416	14894		1.05	1.2E-01	Z21405.1	NT	U1-HB13-adv-10-Q.U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734554 3'
2625	15187	27754	1.38	1.2E-01	AW696556.1	EST_HUMAN	601821567F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:4046224 5'
							Homo sapiens chromosome 21 segment HS21C013
							HSAAAEZT TEST1, Human adult Testis tissue Homo sapiens cDNA
							QV3-BN0046-220300-128-f10 BN0046 Homo sapiens cDNA
							hs18g07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2228988 3' similar to TR:Q14048 Q14048
2754	15309	27875	1.11	1.2E-01	A1623388.1	EST_HUMAN	COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN. [1]. contains element PTR5 repetitive
2869	15486	27859	1.22	1.2E-01	U18018.1	NT	element ;
							Human E1A enhancer binding protein (E1A-F) mRNA, partial cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2927	15543	28019	2.37	1.2E-01	AI720470.1	EST_HUMAN	as80c09.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb:L05095
2961	15577	28056	3.28	1.2E-01	M16384.1	NT	60S RIBOSOMAL PROTEIN L30 (HUMAN);
3037	15653	28132	0.83	1.2E-01	X56882.1	NT	Human creatine kinase-B mRNA, complete cds
3267	15878	28362	2.08	1.2E-01	AW370668.1	EST_HUMAN	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3296	15907		1.19	1.2E-01	U67600.1	NT	QV1-BT0259-261099-021-405 BT0259 Homo sapiens cDNA
3525	16130		0.62	1.2E-01	Z99118.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
3573	16177	28659	0.82	1.2E-01	X56882.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2785131 to 3013540
3573	16177	28660	0.82	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3666	16130		1.09	1.2E-01	Z99118.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3833	16432		0.64	1.2E-01	BF128551.1	EST_HUMAN	Bacillus subtilis complete genome (section 15 of 21); from 2785131 to 3013540
4261	16847	29295	1.98	1.2E-01	Z54255.1	NT	601810789R1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053668 3'
4402	16967	29431	0.6	1.2E-01	M15861.1	NT	P. clarkii mRNA; repeat region (ID 2MR17)
4830	17408	29862	0.98	1.2E-01	Z48183.1	NT	P. clarkii mRNA; repeat region (ID 2MR17)
4909	17484		2.93	1.2E-01	AF221633.1	NT	Chicken neural cell-adhesion molecule (N-CAM) gene, exon 19
5163	17732	30159	1.06	1.2E-01	BF577357.1	EST_HUMAN	L. esculentum mRNA for glycylase-1
5275	17938	30262	10.23	1.2E-01	AL163227.2	NT	Rana ridibunda pituitary adenylate cyclase-activating polypeptide variant 2 precursor, mRNA, complete cds, alternatively spliced
5275	17938	30263	10.23	1.2E-01	AL163227.2	NT	802135185F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4290165 5'
5423	17980		1.99	1.2E-01	AL162757.2	NT	Homo sapiens chromosome 21 segment HS21C027
5457	18092	30408	0.71	1.2E-01	AA744369.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
5503	18137	30547	1.13	1.2E-01	AF223391.1	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome, segment 6/7
5513	18146	30557	2.28	1.2E-01	W33035.1	EST_HUMAN	ny63c04.s1 NCJ_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1282950 3'
5571	18202	30652	2.3	1.2E-01	Z98266.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5696	18322	30822	0.89	1.2E-01	Z48234.1	NT	zc08d02.r1 Soares_papillary_tumor_NbHPA Homo sapiens cDNA clone IMAGE:321698 5'
6347	18952	31731	1.81	1.2E-01	BE020945.1	EST_HUMAN	Homo sapiens gene encoding plakophilin (exons 1-13)
6396	18998	31777	0.81	1.2E-01	P10842	SWISSPROT	M. domestica Borkh. Granny Smith adh mRNA for alcohol dehydrogenase
6441	19043	31831	2.38	1.2E-01	AW845275.1	EST_HUMAN	601493518F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5'
6502	18102	31887	1.59	1.2E-01	M28925.1	NT	MATING-TYPE P-SPECIFIC POLYPEPTIDE P1
6755	19348	32157	0.98	1.2E-01	BF347985.1	EST_HUMAN	IL0-CT0031-221099-113-e04 CT0031 Homo sapiens cDNA
7833	20375		1.31	1.2E-01	BE007072.1	EST_HUMAN	Mouse galactosyltransferase mRNA, complete cds
							602023112F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158386 5'
							PM3-BN0137-280300-002-109 BN0137 Homo sapiens cDNA

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7903	20445	33351	3.58	1.2E-01	AI913753.1	EST_HUMAN	wc99g03.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2328804 3' similar to SW:GST2_HUMAN
7950	20492	33401	0.72	1.2E-01	Q02389	SWISSPROT	Q99735 MICROSOMAL GLUTATHIONE S-TRANSFERASE II ;
8251	20782	33709	0.9	1.2E-01	AI832881.1	EST_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT (COMPLEX I-B22) (CI-B22)
8335	20876		9.03	1.2E-01	AW083852.1	EST_HUMAN	ai71b10.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377435 3'
							xc48d07.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2587597 3' similar to gb:M13452 LAMIN A (HUMAN);
8355	20895						Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
8392	20932	33852	4.17	1.2E-01	AF053772.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8392	20932	33853	0.92	1.2E-01	J03956.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8537	21076		0.92	1.2E-01	J03956.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8623	21162		0.83	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
8657	21196		2.14	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 29 of 163 of the complete genome
9491	21947	34896	0.85	1.2E-01	X15191.1	NT	M.musculus DNA fragment of Apolipoprotein B gene
9918	22414	35389	2.66	1.2E-01	X77961.1	NT	S.cerevisiae HXT5 gene
10155	22650	35644	2.65	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cu Homo sapiens cDNA clone CUAKE08 5'
10768	23280		0.48	1.2E-01	A1718395.1	EST_HUMAN	as59g09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2333056 3'
10944	23460		3.58	1.2E-01	D26184.1	NT	Yeast MPT5 gene for repressor protein, complete cds
11026	23540		3.87	1.2E-01	BE962324.2	EST_HUMAN	601655578R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846283 3'
11134	23642	36882	1.62	1.2E-01	BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
11193	23698	36748	2.67	1.2E-01	AF190493.1	NT	Homo sapiens dynein intermediate chain DNAI1 (DNAI1) gene, exon 17
11382	23834		1.57	1.2E-01	R40249.1	EST_HUMAN	y60c02.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28890 3'
11667	24090		1.8	1.2E-01	M65109.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
12029	24319		4.22	1.2E-01	AV658033.1	EST_HUMAN	AV658033 GLO Homo sapiens cDNA clone GLCF1B12 3'
			4.43	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
12109	25036	30503	3.9	1.2E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)
12228	24447		1.95	1.2E-01	AF188892.1	NT	Drosophila melanogaster strain Oregon R potential RNA-binding protein gene, complete cds; and syntaxin gene, partial cds
12230	13203		17.94	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
12345	24526		1.81	1.2E-01	X33981.1	NT	R.norvegicus NF68 gene for 68kDa neurofilament
12440	24577	30915	6.5	1.2E-01	AJ299903.1	EST_HUMAN	qr20g05.x1 NCI_CGAP_Lu50 Homo sapiens cDNA clone IMAGE:1898840 3'
12463	24591		2.19	1.2E-01	L10187.1	NT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
12468	24972		9.79	1.2E-01	Q96433	SWISSPROT	CYCLIN T

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12649	16130		1.65	1.1E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540
590	13220	25698	0.8	1.1E-01	AI561003.1	EST_HUMAN	h18408.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167983 3'
643	13266	25743	2.98	1.1E-01	AA569008.1	EST_HUMAN	nm08g11.s1 NCI_CGAP_Cot0 Homo sapiens cDNA clone IMAGE:1059820 3' similar to gb:X06985_ma1
1092	13697	26207	1.54	1.1E-01	BF697308.1	EST_HUMAN	HEME OXYGENASE 1 (HUMAN);
1124	13727		1.48	1.1E-01	AL161560.2	NT	602128847F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286771 5'
1201	15435	26314	3.68	1.1E-01	AW972158.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1262	13887	26411	1.89	1.1E-01	D84004.1	NT	EST384142 IMAGE resequences, MAGL Homo sapiens cDNA
1568	14160	26691	2.94	1.1E-01	AU140363.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965
2353	14924		3.72	1.1E-01	6755215	NT	AU140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5'
2578	15401		1.24	1.1E-01	6978676	NT	Mus musculus pre T-cell antigen receptor alpha (Pctra), mRNA
2802	15184		1.06	1.1E-01	AW821809.1	EST_HUMAN	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
2880	15498	27068	1.17	1.1E-01	S82418.1	NT	RCO-ST0379-210100-032-g04 ST0379 Homo sapiens cDNA
3068	15983	28155	0.78	1.1E-01	F03265.1	EST_HUMAN	Interleukin-12 p35 subunit [mouse, Genomic, 700 nt, segment 4 of 5]
3385	15984		1.87	1.1E-01	6753231	NT	HSC1RF02 normalized infant brain cDNA Homo sapiens cDNA clone c-1f02 3'
3468	16075	28548	2.27	1.1E-01	BE393186.1	EST_HUMAN	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Cacna1g), mRNA
3499	16104	28579	1.59	1.1E-01	X62135.1	NT	601308678F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3627068 5'
3538	16143	28626	0.59	1.1E-01	R96946.1	EST_HUMAN	C.reinhardtii nuclear gene on linkage group XIX
3642	16245	28720	0.8	1.1E-01	Y07695.1	NT	y62g08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:200414 3' similar to contains
3763	16364		1.35	1.1E-01	P87384	SWISSPROT	Alu repetitive element;
3771	16372	28837	1.61	1.1E-01	X52708.1	NT	A.immersus gene for transposase
4188	16778	29223	1.61	1.1E-01	AW819412.1	EST_HUMAN	ANNEXIN XI (CALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50)
4188	16778	29224	1.61	1.1E-01	AW819412.1	EST_HUMAN	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4339	16926		12.27	1.1E-01	AF157068.1	NT	MR3-ST0280-290100-025-g07 ST0280 Homo sapiens cDNA
4374	16961	29407	0.63	1.1E-01	AW802056.1	EST_HUMAN	MR3-ST0280-290100-025-g07 ST0280 Homo sapiens cDNA
4745	17326	29768	1.11	1.1E-01	S44957.1	NT	Drosophila melanogaster klarsicht protein (klar) mRNA, complete cds
4958	17533	29975	1.21	1.1E-01	Y07695.1	NT	IL5-UM0070-020500-068-a08 UM0070 Homo sapiens cDNA
							Tapa-1=integral membrane protein TAPA-1 [mouse, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7]
							A.immersus gene for transposase
5169	16784		0.78	1.1E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region/butyrophilin-like protein gene, partial cds;
5431	17988	30392	4.82	1.1E-01	AV730599.1	EST_HUMAN	Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PTT2), CREB-RP, and tenascin X (TNX) genes, complex
5431	17988	30393	4.82	1.1E-01	AV730599.1	EST_HUMAN	AV730599 HTF Homo sapiens cDNA clone HTFAAC12 5'
							AV730599 HTF Homo sapiens cDNA clone HTFAAC12 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5435	18245	28720	0.57	1.1E-01	Y07695.1	NT	A.immersus gene for transposase
5850	18474			1.1E-01	AA747218.1	EST_HUMAN	nx78a03.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1268140 similar to contains Alu repetitive element; contains element MER35 repetitive element
5914	18536	31261	4.49	1.1E-01	AF020927.1	NT	6 Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 6
5974	18594	31328	0.84	1.1E-01	BF339519.1	EST_HUMAN	602039176F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4186818 5'
5974	18594	31329	0.84	1.1E-01	BF339519.1	EST_HUMAN	602039176F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4186818 5'
6001	18621	31358	2	1.1E-01	X68851.1	NT	S.pombe ste8 gene encoding protein kinase
6031	18650	31391	5.02	1.1E-01	M86533.1	NT	Providencia rettgeri penicillin G amidase gene
6177	18787	31555	1.75	1.1E-01	AJ007973.1	NT	Homo sapiens LGMD2B gene
6197	18807	31576	1.6	1.1E-01	BE769152.1	EST_HUMAN	PM3-FT0024-130600-004-f12 FT0024 Homo sapiens cDNA
6216	18828	31598	7.81	1.1E-01	AW853698.1	EST_HUMAN	RC3-GT0254-280989-011-e01 CT0254 Homo sapiens cDNA
6362	19160	31958	1.38	1.1E-01	AF035746.1	EST_HUMAN	AF035746 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43
6399	19106	32001	0.84	1.1E-01	A1216307.1	EST_HUMAN	q976406.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841099 3'
6721	19315	32118	3.92	1.1E-01	O69635	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME)
6805	19396		3.07	1.1E-01	AF032922.1	NT	Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds
6888	19623	32458	2.36	1.1E-01	11432372	NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA
7238	25119		0.97	1.1E-01	BF382759.1	EST_HUMAN	601816524F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4050653 5'
7345	24780	32737	0.92	1.1E-01	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt, position (877)
7542	20062	32935	7.24	1.1E-01	BF884828.1	EST_HUMAN	602140976F1 NIH_MGC 46 Homo sapiens cDNA clone IMAGE:4302019 5'
7542	20062	32936	7.24	1.1E-01	BF884828.1	EST_HUMAN	602140976F1 NIH_MGC 46 Homo sapiens cDNA clone IMAGE:4302019 5'
7651	20163	33051	1.85	1.1E-01	P41067	SWISSPROT	TRAB PROTEIN
7682	20193		0.7	1.1E-01	Z14098.1	NT	B.subtilis gene encoding hypothetical polypeptide synthase
7683	20194	33082					ah31506.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone 1240403 3' similar to gb.J03483
7909	20451	33358	3.53	1.1E-01	AA788784.1	EST_HUMAN	CHROMOGGRANIN A PRECURSOR (HUMAN)
8149	20660	33603	1.41	1.1E-01	U67492.1	NT	Methanococcus jannaschii section 34 of 150 of the complete genome
8149	20660	33604	1.6	1.1E-01	AA493574.1	EST_HUMAN	nh04g10.s1 NCI_CGAP_Thyl Homo sapiens cDNA clone IMAGE:943362
8197	20736	33650	1.18	1.1E-01	X91233.1	NT	nh04g10.s1 NCI_CGAP_Thyl Homo sapiens cDNA clone IMAGE:943362
8235	20776		1.15	1.1E-01	AW817918.1	EST_HUMAN	H.sapiens IL15 gene
8292	20833	33755	1.54	1.1E-01	AL134349.1	EST_HUMAN	PM1-ST0270-080200-001-f09 ST0270 Homo sapiens cDNA
8752	21291	34211	8.48	1.1E-01	U02482.1	NT	DKFZp547P194_r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547P194 5'
8843	21382	34307	0.87	1.1E-01	AI807474.1	EST_HUMAN	Pedococcus acidilactici H plasmid pSMB74 pediocin (pap) gene cluster papA, papB, papC and papD genes, complete cds
							wf48c01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358816 3' similar to contains Alu repetitive element

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8938	21476	34397	0.48	1.1E-01	AF050081.1	NT	Homo sapiens C16orf3 large protein mRNA, complete cds
8973	21511	34433	2.22	1.1E-01	AA192153.1	EST_HUMAN	z993b12.r1 Strategene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
8973	21511	34434	2.22	1.1E-01	AA192153.1	EST_HUMAN	z993b12.r1 Strategene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
9062	21598	34529	0.82	1.1E-01	Y12727.1	NT	P.furiosus partial dph5 gene and argF gene
9092	21628	34565	2.28	1.1E-01	T72875.1	EST_HUMAN	y19h03.s1 Soares fetal liver spleen 1NF1.S Homo sapiens cDNA clone IMAGE:108725 3' similar to
9119	21655		0.67	1.1E-01	BE893260.1	EST_HUMAN	gb:M81181 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
9343	21857		1.13	1.1E-01	BE142305.1	EST_HUMAN	601436672F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922048 5'
9417	21928		2.2	1.1E-01	BF085149.1	EST_HUMAN	CM3-H10142-271089-026-g11 HT0142 Homo sapiens cDNA
9824	22322		0.5	1.1E-01	AL161543.2	NT	MR2-GN0027-040900-005-a08 GN0027 Homo sapiens cDNA
10107	22602		1.03	1.1E-01	R80590.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 43
10240	22735	35727	0.88	1.1E-01	U60529.1	EST_HUMAN	y86a09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147064 3'
10554	23080	36104	1.6	1.1E-01	AF245277.1	NT	Ceratitis capitata yoyo retrotransposon gag-like, pol-like and env-like genes, complete cds
10684	15683	28155	2.12	1.1E-01	F03265.1	EST_HUMAN	Dictyostelium discoideum kinesin Unc104/KIF1a homolog (Unc104) mRNA, complete cds
10802	23325		3.23	1.1E-01	AF169032.1	NT	HSC1R022 normalized infant brain cDNA Homo sapiens cDNA clone c-1r02 3'
10823	23442	36463	3.76	1.1E-01	R23708.1	EST_HUMAN	Carassius auratus activin beta A precursor, mRNA, complete cds
10931	23449	36470	1.85	1.1E-01	6981351	NT	y135f12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131759 5' similar to contains Alu
10947	19597	31298	1.56	1.1E-01	AL110985.1	NT	repetitive element; contains TAR1 repetitive element;
11060	23572	36609	1.74	1.1E-01	X70058.1	NT	Rattus norvegicus Phosphofructokinase, liver, B-type (PFK), mRNA
11085	23597	36633	3.35	1.1E-01	Z11910.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
11085	23597	36634	3.35	1.1E-01	Z11910.1	NT	M.musculus cytokine gene
11186	23691	36738	2.99	1.1E-01	P17437	SWISSPROT	Z.mobilis tgi and lig genes encoding RNA guanine transglycosylase and DNA ligase
11884	24231		4.61	1.1E-01	BE787023.1	EST_HUMAN	Z.mobilis tgi and lig genes encoding RNA guanine transglycosylase and DNA ligase
12143	24835		3.29	1.1E-01	BE974556.1	EST_HUMAN	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
12597	24684	30880	1.99	1.1E-01	BF239753.1	EST_HUMAN	RC2-NT0112-120600-014-003 NT0112 Homo sapiens cDNA
1243	13841		2.35	1.0E-01	O62855	SWISSPROT	601680551R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950804 3'
1315	13909	26429	1.92	1.0E-01	A1995499.1	EST_HUMAN	601908550F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134085 5'
1436	14029	26557	2.23	1.0E-01	AL161504.2	NT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
2531	15095	27667	0.97	1.0E-01	AW451965.1	EST_HUMAN	ws084001.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2496577 3' similar to contains MIER7.03
3563	16167	28649	1.04	1.0E-01	BF033991.1	EST_HUMAN	MER7 repetitive element;
3782	16382	28647	0.82	1.0E-01	BF239618.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
3804	16503	28684	1.41	1.0E-01	AF297061.1	NT	UIH-B13-alc-4-07-0-J1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736420 3'
							601456301F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3959849 5'
							601908489F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5'
							Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3904	16503	28965	1.41	1.0E-01	AF297061.1	NT	Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes
4027	16625	29097	2.82	1.0E-01	BF365703.1	EST_HUMAN	QV2-NT0048-160800-316-e05 NT0048 Homo sapiens cDNA
4496	17080	29529	1.62	1.0E-01	AE002265.2	NT	Chlamydia pneumoniae AR39, section 91 of 94 of the complete genome
4653	17235		0.97	1.0E-01	AI792349.1	EST_HUMAN	an32c04.y6 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4822	17400	29853	1.8	1.0E-01	U60450.1	NT	Drosophila melanogaster tyrosine kinase p45 isoform (fer) mRNA, complete cds
4920	17495	29846	0.96	1.0E-01	AA765434.1	EST_HUMAN	EST384414 IMAGE resequences, MAGB Homo sapiens cDNA
5050	17623	30068	2.12	1.0E-01	AW852344.1	EST_HUMAN	EST384414 HTB Homo sapiens cDNA clone HTBQ10 5'
5408	17965	30375	1.06	1.0E-01	AV721471.1	EST_HUMAN	AV721471 HTB Homo sapiens cDNA clone MDSBQB11 5'
5415	17972		0.88	1.0E-01	AV769960.1	EST_HUMAN	AV769960 MDS Homo sapiens cDNA clone MDSBQB11 5'
5524	18156		8.57	1.0E-01	W88490.1	EST_HUMAN	zh82h04.s1 Soares fetal liver spleen_1NPLS_S1 Homo sapiens cDNA clone IMAGE:416695 3'
6040	18659		0.95	1.0E-01	AK024472.1	NT	Homo sapiens mRNA for FLJ00065 protein, partial cds
6175	18786	31554	11.01	1.0E-01	AF274875.1	NT	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds
6477	19078	31861	0.98	1.0E-01	AA481879.1	EST_HUMAN	zv41g10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:756258 3' similar to contains
6489	19090	31873	0.82	1.0E-01	AA406039.1	EST_HUMAN	L1.13 L1 repetitive element;
7091	19662		1.71	1.0E-01	R23821.1	EST_HUMAN	yz67e12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:743062 3'
7717	20225		2.33	1.0E-01	Y12488.1	NT	yz34h06.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Alu repetitive element;
7874	20416	33324	0.53	1.0E-01	AA861091.1	EST_HUMAN	Mimusculus wln gene
8107	20648		0.6	1.0E-01	4758365	NT	ak32g01.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407698 3' similar to gb:M34182 CAMP-DEPENDENT PROTEIN KINASE, GAMMA-CATALYTIC SUBUNIT (HUMAN);
8429	20969		0.83	1.0E-01	AW189787.1	EST_HUMAN	Homo sapiens fibroblast growth factor 13 (FGF13) mRNA
9113	21649	34590	1.08	1.0E-01	AF102855.2	NT	X09901.x1 NCL CGAP_U4 Homo sapiens cDNA clone IMAGE:2875689 3' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); contains TAR1.3 TAR1 repetitive element;
9416	21925	34873	0.49	1.0E-01	R44963.1	EST_HUMAN	Rattus norvegicus synapto SAPAP-interacting protein Synapton mRNA, complete cds
9426	21935		2.05	1.0E-01	MT6729.1	NT	yz33h04.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34549 3'
9469	21868		2.67	1.0E-01	AE001501.1	NT	Human pro-alpha-1(V) collagen mRNA, complete cds
9483	21940	34898	0.71	1.0E-01	W01955.1	EST_HUMAN	Helicobacter pylori, strain J99 section 62 of 132 of the complete genome
9735	22233	35211	1.67	1.0E-01	BF240154.1	EST_HUMAN	zc66c10.s1 Soares fetal heart_NbH-H19W Homo sapiens cDNA clone IMAGE:327282 3'
9848	22348	35327	8.17	1.0E-01	AB046799.1	NT	601805661F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5'
9848	22346	35328	8.17	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
10048	22543		2.05	1.0E-01	AW957425.1	EST_HUMAN	Homo sapiens mRNA for KIAA1579 protein, partial cds
10053	22548	35542	0.61	1.0E-01	TS1952.1	EST_HUMAN	EST369615 IMAGE resequences, MAGE Homo sapiens cDNA
							yz29a06.s1 Strategene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:72562 3' similar to contains Alu repetitive element

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10234	22729	35720	1.08	1.0E-01	BE792750.1	EST_HUMAN	601584604F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939086 5'
10537	23074		2.11	1.0E-01	AU159127.1	EST_HUMAN	AU159127 THYROT1 Homo sapiens cDNA clone THYROT1000895 3'
10910	23429	38448	3.33	1.0E-01	BF242846.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
10910	23429	38449	3.33	1.0E-01	BF242846.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
11278	23731	36768	5.03	1.0E-01	BE790543.1	EST_HUMAN	601582558F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936734 5'
11870	24581		3.49	1.0E-01	BE537719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451833 5'
12104	24366		1.74	1.0E-01	7682185	NT	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA
12122	24380		1.36	1.0E-01	X00854.1	NT	Drosophila melanogaster ftz gene
12336	24519		2.27	1.0E-01	AA737961.1	EST_HUMAN	nx11008.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1255780 3'
12413	25031		4.74	1.0E-01	U52891.1	NT	Gonyaulax polyedra putative type-1 serine/threonine phosphatase (PP1) mRNA, complete cds
12445	24581		2.17	1.0E-01	BE537719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451833 5'
12495	24623		1.93	1.0E-01	BE158905.1	EST_HUMAN	QV4-HT0401-211289-084-g03 HT0401 Homo sapiens cDNA
12511	25001		41.15	1.0E-01	U68834.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
12578	24874		7.73	1.0E-01	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
2806	15358	27925	0.93	9.9E-02	AF274008.1	NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pke-RII) mRNA, complete cds
2813	15365	27934	1.95	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456385 5'
2813	15365	27935	1.95	9.9E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456385 5'
3305	15916	28393	1.98	9.9E-02	AF089810.1	NT	Homo sapiens neuridin III-alpha gene, partial cds
4025	16623	28095	0.64	9.9E-02	AI821637.1	EST_HUMAN	zu45c03.x5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740932 3'
7049	18068	30459	9.12	9.9E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for blastidin S deaminase, complete cds
7856	20398	33304	0.65	9.9E-02	AW103088.1	EST_HUMAN	xd43c09.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element;
7856	20398	33305	0.65	9.9E-02	AW103088.1	EST_HUMAN	xd43c09.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element;
9181	21758	34704	1.1	9.9E-02	8755111	NT	Mus musculus phospholipid transfer protein (Pltp), mRNA
589	13219		1.48	9.8E-02	X56338.1	NT	O. sativa RAMy3C gene for alpha-amylase
3179	15792	28263	4.23	9.8E-02	AF184274.1	NT	Daucus carota leucoanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4308	16894	29337	8.69	9.8E-02	AF257329.1	NT	Leptosphaeria maculans beta-tubulin mRNA, complete cds
4308	16894	29338	8.69	9.8E-02	AF257329.1	NT	Leptosphaeria maculans beta-tubulin mRNA, complete cds
7495	20018		0.99	9.8E-02	X54133.1	NT	Human HPTP delta mRNA for protein tyrosine phosphatase delta
9178	21755		1.05	9.8E-02	M81943.1	NT	Human laminin B1 chain gene, exon 28
11334	23032	36041	2.27	9.8E-02	BF037421.1	EST_HUMAN	601480793F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864287 5'
11840	24203		1.48	9.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1394	13888	26516	1.24	9.7E-02	AB005808.1	NT	Aloe arborescens mRNA for NADP-malic enzyme, complete cds
1629	14221		1.75	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (echondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2301	14874	27450	2.11	9.7E-02	BE168660.1	EST_HUMAN	QV1-HT0516-070300-085-a04 HT0516 Homo sapiens cDNA
4055	16852		4.76	9.7E-02	Q99795	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5548	18180	30594	1.01	9.7E-02	AF098189.1	NT	Caulobacter crescentus thymidylate kinase (trk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
5548	18180	30595	1.01	9.7E-02	AF098189.1	NT	Caulobacter crescentus thymidylate kinase (trk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
6165	18777	31541	1.29	9.7E-02	AW954478.1	EST_HUMAN	EST366548 IMAGE resequences, MAGO Homo sapiens cDNA
7340	19867	32731	3.26	9.7E-02	Z99119.1	NT	Bacillus subtilis complete genome (section 16 of 21); from 2987771 to 3213410
7924	20466	33374	1.29	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
7924	20466	33375	1.29	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
8783	21322	34246	1.47	9.7E-02	A1953984.1	EST_HUMAN	wx78b06.x1 NCI CGAP_Ov38 Homo sapiens cDNA clone IMAGE:2549747 3' similar to gb:X52851_ma1
11076	23588		2.34	9.7E-02	U58337.1	NT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
2090	14940	27213	1.33	9.6E-02	A1080721.1	EST_HUMAN	Mus musculus ligatin (Lgm) mRNA, partial cds
2090	14940	27214	1.33	9.6E-02	A1080721.1	EST_HUMAN	oz47d11.x1 Soeres_NihHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4437	17023	29463	7.54	9.6E-02	Z32686.2	NT	oz47d11.x1 Soeres_NihHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
5142	17713	30144	1.03	9.6E-02	AW966230.1	EST_HUMAN	Proteus mirabilis fimbrial operon, strain H14320
6254	18863		2.74	9.6E-02	BE910039.1	EST_HUMAN	EST378303 IMAGE resequences, MAGI Homo sapiens cDNA
8317	20858		0.61	9.6E-02	AU137084.1	EST_HUMAN	601498088F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900165 5'
9463	21988	34944	1.34	9.6E-02	AV687898.1	EST_HUMAN	AU137084 PLAGE1 Homo sapiens cDNA clone PLACE1005740 5'
9786	22284		1.35	9.6E-02	BE894895.1	EST_HUMAN	AV687898 GKC Homo sapiens cDNA clone GKGAH02 5'
9852	22447	35429	1.21	9.6E-02	AJ243211.1	NT	601434080F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918363 5'
9852	22447	35430	1.21	9.6E-02	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10055	22550	35544	1.26	9.6E-02	AB013985.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10055	22550	35545	1.26	9.6E-02	AB013985.1	NT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10159	22854	35949	3.43	9.6E-02	P08174	SWISSPROT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10621	23153	36165	7.28	9.6E-02	Z79702.1	NT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD55)
11668	24013	37082	1.81	9.6E-02	AA625755.1	EST_HUMAN	Mycobacterium tuberculosis H37Rv complete genome; segment 102/162
12486	24617		1.55	9.6E-02	H14599.1	EST_HUMAN	zu91g01.s1 Soeres_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
4177	16768	29217	2.24	9.5E-02	AW992395.1	EST_HUMAN	ym19h03.s1 Soeres infant brain 1N1B Homo sapiens cDNA clone IMAGE:48653 3'
5286	17848	30274	1.12	9.5E-02	U63374.1	NT	GM2-BN0023-050200-087-f12 BN0023 Homo sapiens cDNA
							Lycopodium esculentum polygalacturonase isoenzyme 1 beta subunit gene, complete cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5846	18470	31198	0.82	9.5E-02	P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
7344	19871	32736	4.47	9.5E-02	AB003473.1	NT	Trimeresurus flavoviridis DNA for phospholipase A2 inhibitor, complete cds
7589	20086	32963	6.95	9.5E-02	AL181538.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
7885	18470	31198	0.9	9.5E-02	P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
7821	20363	33271	2.04	9.5E-02	BF035881.1	EST_HUMAN	601453642F1 NIH_MGC.66 Homo sapiens cDNA clone IMAGE:3857243 5'
7821	20363	33272	2.04	9.5E-02	BF035881.1	EST_HUMAN	601453642F1 NIH_MGC.66 Homo sapiens cDNA clone IMAGE:3857243 5'
10559	23095	36107	3.19	9.5E-02	BF035881.1	EST_HUMAN	601453642F1 NIH_MGC.66 Homo sapiens cDNA clone IMAGE:3857243 5'
10559	23095	36108	3.19	9.5E-02	BF035881.1	EST_HUMAN	601453642F1 NIH_MGC.66 Homo sapiens cDNA clone IMAGE:3857243 5'
12557	24658		2.4	9.5E-02	AF272732.1	NT	Arabidopsis thaliana putative transcription factor (MYB110) mRNA, complete cds
1873	14459	27015	3.87	9.4E-02	BF671063.1	EST_HUMAN	602150882F1 NIH_MGC.81 Homo sapiens cDNA clone IMAGE:4291917 5'
1804	14489	27050	1.36	9.4E-02	U55944.1	NT	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
1904	14489	27051	1.36	9.4E-02	U55944.1	NT	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
3949	16547	29015	5.59	9.4E-02	Z33059.1	NT	M. capricolum DNA for CONTIG MC073
5383	17942		0.93	9.4E-02	X98106.1	NT	Lactobacillus bacteriophage phi19 complete genomic DNA
6459	19090	31846	0.73	9.4E-02	AF097363.1	NT	Triticum aestivum heat shock protein 101 (Hsp101a) mRNA, complete cds
8536	21075		2.32	9.4E-02	Z46883.1	NT	Acinetobacter sp. cysD, cobQ, cobQ, sodM, lysS, rubA, rubB, estB, oxyR, ppk, mtaA, ORF2 and ORF3 genes
10813	20107	32982	2.33	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and vail genes, complete cds, and ipf35 gene, partial cds
11722	24934		8.48	9.4E-02	U31815.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
12845	24719	30869	3.54	9.4E-02	U27896.1	NT	Human pepHGT-1 betaine-GABA transporter mRNA, complete cds
3018	15634		1.66	9.3E-02	4809280	NT	Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA
3063	15679		7.31	9.3E-02	6912525	NT	Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA
3295	15906	28387	2.05	9.3E-02	BF575511.1	EST_HUMAN	602133086F1 NIH_MGC.81 Homo sapiens cDNA clone IMAGE:4288269 5'
4232	16820	29269	4.11	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC.44 Homo sapiens cDNA clone IMAGE:3607653 5'
4232	16820	29270	4.11	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC.44 Homo sapiens cDNA clone IMAGE:3607653 5'
4840	17418		1.28	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAUA08 5'
5843	18487		0.73	9.3E-02	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
8190	20731	33643	0.52	9.3E-02	AW568007.1	EST_HUMAN	EST68 Human Fetal Brain MATCHMAKER cDNA Library Homo sapiens cDNA
9052	21589		0.5	9.3E-02	AL113179.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9626	22126	35090	2.1	9.3E-02	BE962631.2	EST_HUMAN	601655888R1 NIH_MGC.66 Homo sapiens cDNA clone IMAGE:3855981 3'
10094	22589	35581	3.16	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10094	22589	35582	3.16	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10222	22717		3.82	9.3E-02	AW206117.1	EST_HUMAN	U1H-B11-afx-h-05-o-UJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723553 3'
11892	24854		2.27	9.3E-02	AJ248850.1	NT	Photobacterium damselae subsp. damselae partial gyrB gene for DNA gyrase B subunit

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12379	24886		18.03	9.3E-02	AW468850.1	EST_HUMAN	hd28h12.1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810887 3'
12599	24933						Mus musculus major histocompatibility locus class II region, Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl t>
249	12909	25390	3.18	9.3E-02	AF100958.1	NT	
249	12909	25391	5.24	9.2E-02	U60315.1	NT	
249	12909	25392	5.24	9.2E-02	U60315.1	NT	
249	12909	25392	5.24	9.2E-02	U60315.1	NT	
2269	14843		1.58	9.2E-02	R54156.1	EST_HUMAN	Mollusum contagiosum virus subtype 1, complete genome
3213	15825	28302	3.92	9.2E-02	Q2863.1	SWISSPROT	Mollusum contagiosum virus subtype 1, complete genome
3345	15955	28430	0.86	9.2E-02	AA534354.1	EST_HUMAN	Mollusum contagiosum virus subtype 1, complete genome
3646	16249		1.16	9.2E-02	8755215	NT	Major EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
4322	16908		1.42	9.2E-02	U92048.1	NT	Major EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
4396	16981		0.85	9.2E-02	BE299722.1	EST_HUMAN	Major EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
4744	17325	29767	1.44	9.2E-02	X96402.1	NT	Major EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
7951	20493	33402	1.75	9.2E-02	T49920.1	EST_HUMAN	Major EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
8117	20658	33567	2.11	9.2E-02	X95256.1	NT	Major EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
12656	24930		2.09	9.2E-02	Z22150.1	NT	Major EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
448	12677	25134	2.83	9.1E-02	X77685.1	NT	Major EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3733	16334		0.95	9.1E-02	AW372569.1	EST_HUMAN	Major EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
4582	17165	29608	1.55	9.1E-02	AL161554.2	NT	Major EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
5905	18527	31253	1.5	9.1E-02	AF129756.1	NT	Major EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
7420	19944	32809	11.98	9.1E-02	AW160658.1	EST_HUMAN	Major EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
7668	20180	33067	0.89	9.1E-02	AP000081.1	NT	Major EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
7695	20204	33091	0.68	9.1E-02	U39073.1	NT	Major EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
8855	21394	34317	1.05	9.1E-02	Y14379.1	NT	Major EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
10325	22819		1.39	9.1E-02	T02884.1	EST_HUMAN	Major EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
10354	22848	35842	1.52	9.1E-02	S74059.1	NT	Major EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
10380	22874	35867	0.73	9.1E-02	Y11187.1	NT	Major EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
11656	24083		2.35	9.1E-02	9633494	NT	Major EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
11898	25036		1.82	9.1E-02	AA179801.1	EST_HUMAN	Major EPIDIDYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11978	24289		2.21	9.1E-02	AF032685.1	NT	Rattus norvegicus cell cycle protein p55CDC gene, complete cds
12487	24877		17.53	9.1E-02	AJ291390.1	NT	Homo sapiens partial MUC3B gene for MUC3B mucin, exons 1-11
12672	24740		1.5	9.1E-02	AF226888.1	NT	Bombyx mori fibroin heavy chain Fib-H (fib-H) gene, complete cds
774	13393	25893	3.92	9.0E-02	P15328	SWISSPROT	FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
1676	14268	26901	6.34	9.0E-02	BE220482.1	EST_HUMAN	h09g10.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element;
2826	15381	27951	1.76	9.0E-02	AF138522.1	NT	HIV-1 p8c085-06 from USA envelope glycoprotein (env) gene, partial cds
2829	15381	27952	1.76	9.0E-02	AF138522.1	NT	HIV-1 p8c086-06 from USA envelope glycoprotein (env) gene, partial cds
3380	15989	28488	0.83	9.0E-02	AF279135.1	NT	Dictyostelium discoideum spore coat structural protein SP65 (colE) gene, complete cds
4387	16973	29422	0.59	9.0E-02	S68757.1	NT	corticosteroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4387	16973	29423	0.59	9.0E-02	S68757.1	NT	corticosteroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4775	17356	29808	1.68	9.0E-02	X65740.2	NT	Plasmodium falciparum P-type A TPase 3 gene
5401	17959	30370	1.12	9.0E-02	Q24597	SWISSPROT	REGULATORY PROTEIN ZESTIE
6146	18760	31519	18.48	9.0E-02	W56037.1	EST_HUMAN	z688a12.r1 Soares_fetal_lung_NBHL19W Homo sapiens cDNA clone IMAGE:297684 5' similar to PIR:S62171 S62171 small G protein - human ;
6820	19410		1.1	9.0E-02	BF062651.1	EST_HUMAN	7h63d03.x1 NCL_CGAP_Cot6 Homo sapiens cDNA clone IMAGE:3320845 3' similar to contains Alu repetitive element;
6864	19508	32428	0.77	9.0E-02	R62805.1	EST_HUMAN	yf11508.s1 Soares_placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
12300	24497		2.42	9.0E-02	AF022236.1	NT	Escherichia coli strain E2348/69 pathogenicity island, rOrf1 (rOrf1), rOrf2 (rOrf2), EscR (escR), EscS (escS), EscT (escT), EscU (escU), CesD (cesD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscV (escV), EscN (escN), SepQ (sepQ), Tir (tir), OriU (oriU), >
1486	14079	26617	1.46	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
1486	14079	26618	1.46	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
2430	14997	27571	9.68	8.9E-02	BE153572.1	EST_HUMAN	PM0-HT0339-251199-003-d01 HT0339 Homo sapiens cDNA
4277	16863		1.79	8.9E-02	AF286055.1	NT	Atrichum angustatum AtranFlo2 protein (AtranFlo2) gene, partial cds
4741	17322	29782	1.91	8.9E-02	AA424897.1	EST_HUMAN	zw03d04.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:768166 3'
6014	18634	31370	3.35	8.9E-02	AW452122.1	EST_HUMAN	UI-H-B13-alc-f-08-Q-UI.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
6014	18634	31371	3.35	8.9E-02	AW452122.1	EST_HUMAN	UI-H-B13-alc-f-08-Q-UI.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
6026	18845	31387	3.24	8.9E-02	11433478	NT	Homo sapiens similar to endoglycan (H. sapiens) (LOC63107), mRNA
7244	19773	32630	1.76	8.9E-02	P47259	SWISSPROT	FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE ; METHENYL-TETRAHYDROFOLATE CYCLOHYDROLASE]
7559	20077		2.15	8.9E-02	Z76021.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA20F8

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7994	20536	33439	0.99	8.9E-02	P29475	SWISSPROT	NITRIC-OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS) (CONSTITUTIVE NOS) (NC-NOS) (BNOS)
8072	20614	33528	0.69	8.9E-02	BF701665.1	EST_HUMAN	602129111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
8072	20614	33529	0.69	8.9E-02	BF701665.1	EST_HUMAN	602129111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
8534	21073	33693	4.81	8.9E-02	AA309319.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
9538	22038	34998	0.83	8.9E-02	AI285627.1	EST_HUMAN	qu55c05.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1968680 3' similar to contains MER10.b1 MER10 repetitive element;
9538	22038	34999	0.83	8.9E-02	AI285627.1	EST_HUMAN	qu55c05.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1968680 3' similar to contains MER10.b1 MER10 repetitive element;
9648	22147	35118	0.55	8.9E-02	AA339356.1	EST_HUMAN	EST44454 Fetal brain 1 Homo sapiens cDNA 5' end
11721	24884		2.61	8.9E-02	P19524	SWISSPROT	MYOSIN-2 ISOFORM
11872	24224		4.62	8.9E-02	BF696918.1	EST_HUMAN	602129682F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286180 5'
12044	24330		3.07	8.9E-02		NT	Mus musculus hippocampus abundant gene transcript 1 (Hla1), mRNA
12307	25104		1.57	8.9E-02	U40493.1	NT	Ceratitis capitata mariner transposase gene, complete cds
1416	14009	29538	1.36	8.8E-02	Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
3971	16569	29038	1.08	8.8E-02	AA299128.1	EST_HUMAN	EST11595 Uterus Homo sapiens cDNA 5' end
4106	16700		4.3	8.8E-02	Q00268	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT (TAFII135) (TAFII130)
4390	16976		0.96	8.8E-02	4580423	NT	Homo sapiens paired box gene 6 (aniridia, keratitis) (PAX6), isoform b, mRNA
8918	21456	34376	1.18	8.8E-02	AA151872.1	EST_HUMAN	zr99a05.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:566288 3'
10997	23511	36543	3.11	8.8E-02	BE264455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
10997	23511	36544	3.11	8.8E-02	BE264455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
11142	23650	36692	10.91	8.8E-02	AL040129.1	EST_HUMAN	DKFZ434D1313 t1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D1313 5'
11948	24277	31019	1.73	8.8E-02	Z71561.1	NT	S.cerevisiae chromosome XIV reading frame ORF YNL285w
3756	16357	28826	3.9	8.7E-02	U82995.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3756	16357	28827	3.9	8.7E-02	U82995.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4816	17394	28847	1.42	8.7E-02	AF178636.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5264	17826		1.2	8.7E-02	AE000895.1	NT	Methanobacterium thermoautotrophicum from bases 1176181 to 1189406 (section 101 of 148) of the complete genome
5517	18149	30561	5.18	8.7E-02	AA286875.1	EST_HUMAN	z355g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5517	18149	30562	5.18	8.7E-02	AA286875.1	EST_HUMAN	z559p08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
6931	19590	32421	0.75	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
6931	19590	32422	0.75	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
7803	20346		0.46	8.7E-02	AA284532.1	EST_HUMAN	z120e03.s1 Soares ovary tumor NbrHOT Homo sapiens cDNA clone IMAGE:713692 3'
8452	20992	33910	0.64	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PA01, section 348 of 529 of the complete genome
8452	20992	33911	0.64	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PA01, section 348 of 529 of the complete genome
10590	23125		2.71	8.7E-02	L04758.1	NT	Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' end
11191	23696	38745	1.77	8.7E-02	AJ007763.1	NT	Glucobacter oxydans (RNA-1) and (RNA-1a) genes
11835	24289		2.35	8.7E-02	X17116.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
12142	24389		2.72	8.7E-02	6679057	NT	Mus musculus nidogen 2 (Nid2), mRNA
1295	13989	28412	6.51	8.6E-02	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
2286	14860	27435	2.47	8.6E-02	BE408687.1	EST_HUMAN	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638643 5'
3222	15934	28312	2.42	8.6E-02	L05488.1	NT	Trichomonas vaginalis beta-tubulin (tub1) gene, complete cds
3708	16307		4.02	8.6E-02	AF153362.1	NT	Dictyostelium discoideum adenyl cyclase (acrA) gene, complete cds
4594	17167	29610	0.59	8.6E-02	U68179.1	NT	Oryctolagus cuniculus galectin-3 gene, untranslated exon and 5' flanking region
6244	18953	31624	5.78	8.6E-02	Y10928.1	NT	Homo sapiens LCN1b gene
6512	19112	31899	1.56	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
6512	19112	31900	1.56	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
7581	20098	32974	1.14	8.6E-02	P14616	SWISSPROT	INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED RECEPTOR)
7871	20413	33319	1.23	8.6E-02	5730066	NT	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA
7871	20413	33320	1.23	8.6E-02	5730066	NT	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA
8015	20557	33460	0.76	8.6E-02	11427428	NT	Homo sapiens hypodermal protein FLJ11008 (FLJ11008), mRNA
8073	20615		0.65	8.6E-02	U60188.1	NT	Dictyostelium discoideum proteasome subunit C2 homolog Ptc (ptc) gene, complete cds
9852	22151	35121	1.18	8.6E-02	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
9888	22187		1.27	8.6E-02	AW662153.1	EST_HUMAN	h120e08.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872848 3'
10057	22552	35547	0.74	8.6E-02	AF026504.1	NT	Rattus norvegicus SPA-1 like protein p1294 mRNA, complete cds
10824	23345	36360	1.68	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
10824	23345	36361	1.68	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11128	23636	36677	4.74	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11128	23636	36678	4.74	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11315	23013	36022	7.58	8.6E-02	AE001073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
2440	15007	27579	2.52	8.5E-02	AE000652.1	NT	Helicobacter pylori 26895 section 130 of 134 of the complete genome

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5885	18507		1.91	8.5E-02	P08089	SWISSPROT	M PROTEIN, SEROTYPE 6 PRECURSOR
8162	18775	31537	5.64	8.5E-02	AF233885.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds
8842	21081	34002	1.78	8.5E-02	6754779	NT	Mus musculus myosin XV (Myo15), mRNA
9750	22248	35230	3.08	8.5E-02	BE833054.1	EST_HUMAN	RC4-O T0037-200700-014-e05 OT0037 Homo sapiens cDNA
9750	22248	35231	3.08	8.5E-02	BE833054.1	EST_HUMAN	RC4-O T0037-200700-014-e05 OT0037 Homo sapiens cDNA
10378	22873	35666	0.92	8.5E-02	11418108	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
11035	23549		12.56	8.5E-02	AF155510.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
11050	23563	36598	4.42	8.5E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
12354	24814		5.89	8.5E-02	AJ005586.1	NT	Antirrhinum majus mRNA for MYB-related transcription factor
12536	24847		2.27	8.5E-02	AA362834.1	EST_HUMAN	EST72736 Ovary II Homo sapiens cDNA 5' end
2890	15474	27816	3.71	8.4E-02	W69330.1	EST_HUMAN	z044e1.1.1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:343532 5'
5200	17765		1	8.4E-02	X01472.1	NT	Drosophila melanogaster copia-like element 17.6
5369	17929	30343	0.88	8.4E-02	5453817	NT	Homo sapiens nucleobindin 1 (NUCB1), mRNA
5515	18147	30559	9.46	8.4E-02	BE287153.1	EST_HUMAN	601190436F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3534393 5'
8791	19382	32197	1.67	8.4E-02	AK024458.1	NT	Homo sapiens mRNA for FLJ00050 protein, partial cds
7972	20514	33421	7.35	8.4E-02	BE095074.1	EST_HUMAN	CM3-B T0780-280400-182-d05 BT0780 Homo sapiens cDNA
8776	21315	34237	1.13	8.4E-02	AF218890.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 2
10285	22760	35747	1.61	8.4E-02	AI735184.1	EST_HUMAN	as88g10.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335842 3' similar to TR:O88312
11858	24217	31042	1.92	8.4E-02	R79408.1	EST_HUMAN	O88312 GOB-4 ;
2056	14637	27208	2.06	8.3E-02	5835680	NT	y83h12.1.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145895 5'
2058	14637	27209	2.06	8.3E-02	5835680	NT	ixodes hexagonus mitochondrion, complete genome
3652	16255	28728	8.98	8.3E-02	P75334	SWISSPROT	ixodes hexagonus mitochondrion, complete genome
3680	16281	28748	0.68	8.3E-02	AI436797.1	EST_HUMAN	HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR
3680	16281	28749	0.68	8.3E-02	AI436797.1	EST_HUMAN	ih82g06.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
5416	17973		1.71	8.3E-02	AW902857.1	EST_HUMAN	ih82g06.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
8408	19009	31781	0.89	8.3E-02	AI942338.1	EST_HUMAN	QV3-NN1025-030500-173-e04 NN1025 Homo sapiens cDNA
6504	19104	31889	3.05	8.3E-02	AF052683.1	NT	w078r11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2461581 3'
7922	20464	33371	3.57	8.3E-02	AF195787.1	NT	Homo sapiens protocadherin 43 gene, exon 1
7955	20497		1.31	8.3E-02	AA865285.1	EST_HUMAN	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Dp2) mRNA, complete cds
8241	20782		4.14	8.3E-02	AA987873.1	EST_HUMAN	og88g08.s1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1455422 3' similar to contains L1.t1 L1 L1 repetitive element
9457	21983	34935	1.55	8.3E-02	AW583503.1	EST_HUMAN	oq81f10.s1 NCL_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1592779 3'
							ia05h10.x1 Human Pancreatic islets Homo sapiens cDNA 3' similar to TR:Q15332 Q15332 GAMMA
							SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE. ;

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9470	21869		1.94	8.3E-02	AL181595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
10244	22739		0.56	8.3E-02	AF020409.1	NT	Dictyostelium discoideum DocA (docA) mRNA, complete cds
11550	23998	37070	1.7	8.3E-02	AA700756.1	EST_HUMAN	262004.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435367 3' similar to contains element MER22 repetitive element:
11953	25040		1.36	8.3E-02	BE958458.1	EST_HUMAN	601844770F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3928983 5'
1421	14014		9.32	8.2E-02	Y08170.2	NT	Gallus gallus mRNA for OBCAM protein gamma isoform
1542	14134	26668	1.79	8.2E-02	AF167077.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
3109	15724		2.23	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
3874	16472		1.66	8.2E-02	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4079	16675	29136	1.29	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
4371	16958	29400	7.78	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4371	16958	29401	7.76	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4371	16958	29402	7.76	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5240	17804	30225	3.53	8.2E-02	U76009.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
5400	17958	30369	0.9	8.2E-02	AU119830.1	EST_HUMAN	AU119830 HEMBA1 Homo sapiens cDNA clone HEMBA1006744 5'
5538	18170	30585	1.62	8.2E-02	BE897030.1	EST_HUMAN	601439576F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924523 5'
7092	19663	32502	3.11	8.2E-02	AF309555.1	NT	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
8707	21248	34169	2.98	8.2E-02	AW875126.1	EST_HUMAN	RC2-PT0004-031289-011-405 PT0004 Homo sapiens cDNA
9517	22017	34974	4.96	8.2E-02	X04197.1	NT	Beet necrotic yellow vein virus RNA-2
9678	22177	35152	2.2	8.2E-02	BE254318.1	EST_HUMAN	601115055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355596 5'
11959	24281	31023	5.69	8.2E-02	AE002246.2	NT	Chlamydia pneumoniae AR39, section 73 of 94 of the complete genome
12383	24806		4.6	8.2E-02	AF275386.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
5929	18551	31278	1.08	8.1E-02	AE004006.1	NT	Xylella fastidiosa, section 152 of 229 of the complete genome
6516	19116	31906	0.97	8.1E-02	T11532.1	EST_HUMAN	A1484F Heart Homo sapiens cDNA clone A1484
7248	19177		0.72	8.1E-02	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
7582	20097		1.03	8.1E-02	AI692681.1	EST_HUMAN	wd8608.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2338503 3'
8281	20822	33741	0.62	8.1E-02	11426974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
8281	20822	33742	0.62	8.1E-02	11426974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
9826	23224		1.7	8.1E-02	A005150.1	NT	Homo sapiens extracellular glycoprotein lacritin precursor, gene, complete cds
11371	23823	36886	1.87	8.1E-02	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
6	15405	25143	9.1	8.0E-02	AW954653.1	EST_HUMAN	EST1968723 MAGE resequences, MAGEC Homo sapiens cDNA
971	13582	26095	1.13	8.0E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
1736	15449	28869	10.86	8.0E-02	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1736	15449	26870	10.88	8.0E-02	D28535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
1947	14531	27087	3.32	8.0E-02	BE067219.1	EST_HUMAN	PM3-BT0347-170200-001-b08 BT0347 Homo sapiens cDNA
2413	14981	27556	1.14	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2413	14981	27557	1.14	8.0E-02	D90915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2508	15073		4.66	8.0E-02	BF246744.1	EST_HUMAN	601855548FT NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075619.5
2847	13733	26243	0.87	8.0E-02	M23449.1	NT	Dictyosailum discoideum cyclic nucleotide phosphodiesterase gene, complete cds
2825	15541	28016	0.84	8.0E-02	AL445067.1	NT	Thermoplasma acidophilum complete genome, segment 5/5
3888	16487	28948	0.59	8.0E-02	AW966118.1	EST_HUMAN	EST378197 IMAGE resequences, MAGI Homo sapiens cDNA
4148	18738		0.95	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
4890	17465	29920	2.28	8.0E-02	AI434202.1	EST_HUMAN	t131g02.x1 NCJ_GGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132114.3
4939	17514		5.81	8.0E-02	X72794.1	NT	M.musculus gene for gelatinase B
6051	18669	31408	3.07	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7232	18669	31408	1.42	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8069	20611	33524	3.68	8.0E-02	AL114993.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9311	21825	34773	1.22	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
9311	21825	34774	1.22	8.0E-02	X74208.1	NT	H. sapiens AGT gene, intron 4
10063	22558		0.57	8.0E-02	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
10871	23203	36216	3.69	8.0E-02	AF217798.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
11993	24302	30988	3.6	8.0E-02	AJ005375.1	NT	Drosophila arena hunchback region
12595	16738		3.88	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
2218	14793	27366	4.15	7.9E-02	BE250008.1	EST_HUMAN	600943191FT NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2895610.5
3007	15623	28101	11.7	7.9E-02	AI582029.1	EST_HUMAN	ar98c08.x1 Barslead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173646.3' similar to gb:226876
							60S RIBOSOMAL PROTEIN L38 (HUMAN);
							Plasmodium falciparum strain Da2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), putative chloroquine resistance transporter (crt), CG8 (cg8), CG1 (cg1), CG6 (cg6), CG2 (cg2), and CG7 (cg7) genes, complete cds
3865	16463	28927	0.92	7.9E-02	AF030694.2	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
3917	16515	28978	3	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
3917	16515	28979	3	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4934	17509		1.36	7.9E-02	AB008019.1	NT	Arabidopsis thaliana RXW24L mRNA, partial cds
5390	17948	30360	0.58	7.9E-02	AF035672.1	NT	Mus musculus MHC class I related protein 1 (MR1) gene, complete cds
5390	17948	30361	0.58	7.9E-02	AF035672.1	NT	Mus musculus MHC class I related protein 1 (MR1) gene, complete cds
6798	19389		1.08	7.9E-02	BF368016.1	EST_HUMAN	RC3-GN0042-310800-024-d11 GN0042 Homo sapiens cDNA
7975	20517	33424	3.32	7.9E-02	U27832.1	NT	Saccharomyces cerevisiae suppressor of Mif2 Smt4p (SMT4) gene, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9941	22436	35412	4.71	7.9E-02	A081844.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP.C37A2.2 CE08611;
9941	22436	35413	4.71	7.9E-02	A081844.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP.C37A2.2 CE08611;
12479	24613		1.42	7.9E-02	A1761839.1	EST_HUMAN	wg66h01.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370097 3'
1252	13849	26365	1.36	7.8E-02	A1793275.1	EST_HUMAN	oo58d02.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570487 5' similar to contains L1.13 L1 repetitive element;
1252	13849	26366	1.36	7.8E-02	A1793275.1	EST_HUMAN	oo58d02.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570487 5' similar to contains L1.13 L1 repetitive element;
4912	17487	26943	0.67	7.8E-02	BE836331.1	EST_HUMAN	PM3-FN0058-140700-005-109 FN0058 Homo sapiens cDNA
5247	18412		2.77	7.8E-02	BE250048.1	EST_HUMAN	600943055F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:2856693 5'
7138	19475	32297	1.34	7.8E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
7138	19475	32298	1.34	7.8E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8720	21259	34179	1.46	7.8E-02	BE897847.1	EST_HUMAN	601440439F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925449 5'
8813	21352	34274	0.6	7.8E-02	X78344.1	NT	S. cerevisiae CAT8 gene
8983	21521	34447	0.83	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
8983	21521	34448	0.83	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1b mRNA, complete cds
9283	21883	34828	1.08	7.8E-02	AA469354.1	EST_HUMAN	nc68b08.f1 NCI_CGAP_Pt1 Homo sapiens cDNA clone IMAGE:771731
9717	22215	35189	0.5	7.8E-02	Z99124.1	NT	Bacillus subtilis complete genome (section 21 of 21): from 3999281 to 4214814
10544	23081	36094	1.67	7.8E-02	U32323.1	NT	Human interleukin-11 receptor alpha chain gene, complete cds
12384	24550	30908	1.95	7.8E-02	U72847.1	NT	Homo sapiens enovoplakin (EVPL) gene, exons 15 through 18
1444	15442	26566	0.91	7.7E-02	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
3647	18250		2.62	7.7E-02	AJ238063.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
5129	17701	30135	0.92	7.7E-02	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
7850	20392	33295	5.56	7.7E-02	AA402949.1	EST_HUMAN	zu53d11.1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:741717 5' similar to TR:G1173905 G1173905 SPLICEOSOME ASSOCIATED PROTEIN.;
9749	22247	35229	5.97	7.7E-02	P38080	SWISSPROT	PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10037	22932	35527	0.75	7.7E-02	AI318662.1	EST_HUMAN	ta80b08.x1 NCI CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z28876 60S
10037	22932	35528	0.75	7.7E-02	AI318662.1	EST_HUMAN	RIBOSOMAL PROTEIN L38 (HUMAN);
10889	23410	36428	4.97	7.7E-02	11422757	NT	ta80b08.x1 NCI CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z28876 60S
12194	24894		1.91	7.7E-02	11439859	NT	RIBOSOMAL PROTEIN L38 (HUMAN);
3434	16042	28523	3.08	7.6E-02	BE514432.1	EST_HUMAN	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
3455	16062	28537	0.67	7.6E-02	AA298447.1	EST_HUMAN	Homo sapiens interferon regulatory factor 7 (IRF7), mRNA
3615	16218	28697	0.67	7.6E-02	AJ400877.1	NT	601316426F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903 5'
4993	17567		2.04	7.6E-02	AW858844.1	EST_HUMAN	EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to similar to protocadherin 43
6247	18856	31627	0.7	7.6E-02	AI061275.1	EST_HUMAN	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6497	19098	31862	0.83	7.6E-02	BE379328.1	EST_HUMAN	RC3-CT0347-110300-014-a05 CT0347 Homo sapiens cDNA
9292	21892	34839	1.24	7.6E-02	AJ131016.1	NT	an2502.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1699730 3'
9811	22309		1.7	7.6E-02	AL139078.2	NT	601236402F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608401 5'
10120	22615	36605	0.52	7.6E-02	BE708002.1	EST_HUMAN	Homo sapiens SCL gene locus
10251	22746		0.49	7.6E-02	BE959638.2	EST_HUMAN	Campylobacter jejuni NCTC11168 complete genome; segment 5/6
10480	22974	35981	0.72	7.6E-02	X92656.1	NT	RC1-HT0545-020800-017-d06 HT0545 Homo sapiens cDNA
10480	22974	35982	0.72	7.6E-02	X92656.1	NT	601654915R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839810 3'
11526	23974	37044	2.58	7.6E-02	AW996645.1	EST_HUMAN	L. esculentum mRNA for triose phosphate translocator
817	13435	25940	1.18	7.5E-02	5902093	NT	L. esculentum mRNA for triose phosphate translocator
817	13435	25941	1.18	7.5E-02	5902093	NT	QV3-BN0046-150400-151-a04 BN0046 Homo sapiens cDNA
4606	17188	29636	0.57	7.5E-02	AB015961.1	NT	Homo sapiens solute carrier family 8 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
8280	20821	33740	1.15	7.5E-02	A1864367.1	EST_HUMAN	Homo sapiens solute carrier family 8 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
8444	20984	33899	1.18	7.5E-02	AU116913.1	EST_HUMAN	Homo sapiens IL-18 gene for Interleukin-18, intron 1 and exon 2
9945	22440		0.5	7.5E-02	BF221730.1	EST_HUMAN	w52602.x1 NCI CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:M14328 ALPHA ENOLASE (HUMAN);
10387	22851	35875	0.9	7.5E-02	BF206809.1	EST_HUMAN	AU116913 HEMBA1 Homo sapiens cDNA clone HEMBA1000264 5'
10481	22975	35983	0.71	7.5E-02	X79460.1	NT	7c61c05.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:3576504 3' similar to contains element MER27 repetitive element;
503	13135	25623	1.23	7.4E-02	AW839547.1	EST_HUMAN	601870205F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100449 5'
1509	14101		0.97	7.4E-02	AF030027.1	NT	C.fimi DSM 20113 16S rDNA
							RG5-L T0054-260100-011-H09 L T0054 Homo sapiens cDNA
							Equine herpesvirus 4 strain NS80567, complete genome

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2616	15178		1.04	7.4E-02	6755069	NT	Mus musculus paired-like homeodomain transcription factor 1 (Pbx1), mRNA
3654	16257	28729	0.84	7.4E-02	AI807885.1	EST_HUMAN	wf43h01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358385 3'
4814	17392	28844	1.33	7.4E-02	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4911	17486	28942	2.82	7.4E-02	6978442	NT	Rattus norvegicus Actin receptor like kinase 1 (Acvrl1), mRNA
5052	17625		1.65	7.4E-02	AE000898.1	NT	Methanobacterium thermoautotrophicum from bases 1076134 to 1086763 (section 92 of 148) of the complete genome
5076	17649	30090	1.87	7.4E-02	6678492	NT	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchrrp), mRNA
5393	17951	30384	0.93	7.4E-02	AJ012469.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6621	19218		1.84	7.4E-02	R17477.1	EST_HUMAN	yp14g06.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:32339 5'
7485	20008	32874	0.68	7.4E-02	AA605132.1	EST_HUMAN	nc71d02.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112259 3'
7842	20384	33288	1.23	7.4E-02	BE880112.1	EST_HUMAN	601493386F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3885284 5'
8438	20978	33893	1.2	7.4E-02	U56089.1	NT	Human periodic tyrophen protein 2 (PWP2) gene, exons 15 to 21, and complete cds
9093	21628	34566	0.92	7.4E-02	AW629605.1	EST_HUMAN	hh67d11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2667861 5' similar to SW:SCA2_HUMAN
9093	21628	34566	0.92	7.4E-02	AW629605.1	EST_HUMAN	hh67d11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2667861 5' similar to SW:SCA2_HUMAN
9360	20299	33197	0.72	7.4E-02	AI672939.1	EST_HUMAN	O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2 ;
9360	20299	33198	0.72	7.4E-02	AI672939.1	EST_HUMAN	O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2 ;
9728	22228	35203	0.85	7.4E-02	U62293.1	NT	we74d02.x1 Soares_Dieckgrafe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3'
11600	24043		1.57	7.4E-02	U89282.1	NT	we74d02.x1 Soares_Dieckgrafe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3'
11912	24250		1.29	7.4E-02	11525893	NT	Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds
12187	25015		4.44	7.4E-02	AW379431.1	EST_HUMAN	Rattus norvegicus telomerase protein component 1 (TLP1) mRNA, complete cds
12351	24531	30926	2.8	7.4E-02	BF035099.1	EST_HUMAN	Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA
12361	24535	30901	1.37	7.4E-02	AJ223499.2	NT	CM4-HT0243-081199-037-d11 HT0243 Homo sapiens cDNA
494	13127	25613	1.42	7.3E-02	BE584981.2	EST_HUMAN	601453813F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3857738 5'
494	13127	25614	1.42	7.3E-02	BE584981.2	EST_HUMAN	Aspergillus nidulans prnD, prnX, prnA genes
713	13334	25820	2.68	7.3E-02	AE001789.1	NT	601658739R1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3886209 3'
1528	15444	26659	4.47	7.3E-02	AW900281.1	EST_HUMAN	601658739R1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3886209 3'
1885	15453		16.16	7.3E-02	AL163302.2	NT	Thermotoga maritima section 101 of 136 of the complete genome
							CM05-NN1004-130300-284-g08 NN1004 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C102
							Human gemline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV8S1A1T, TCRBV7S1A1N2T, TCRBV6S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV6S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
3838	16437		0.59	7.3E-02	U66059.1	NT	
5137	17709		1.11	7.3E-02	U12283.1	NT	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6580	19178	31978	1.56	7.3E-02	AA79877.1	EST_HUMAN	z24a02.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to
7484	20007	32872	4.36	7.3E-02	P05143	SWISSPROT	gbL02426 26S PROTEASE SUBUNIT 4 (HUMAN);
7484	20007	32873	4.36	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8109	20650		1.06	7.3E-02	7662107	NT	PROLINE-RICH PROTEIN MP-3
9137	21672		1.38	7.3E-02	AB011080.1	NT	Homo sapiens KIAA0424 protein (KIAA0424), mRNA
							Homo sapiens mRNA for KIAA0518 protein, partial cds
11085	19178	31978	3.07	7.3E-02	AA79877.1	EST_HUMAN	z24a02.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to
							gbL02426 26S PROTEASE SUBUNIT 4 (HUMAN);
125	12794	25279	1.36	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
125	12784	25280	1.36	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
1524	14116	26652	2.11	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
1524	14116	26653	2.11	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2585	15148		2.76	7.2E-02	U14794.1	NT	Homo sapiens immunodeficiency virus type 1 isolate 26 reverse transcriptase (pol) gene, internal fragment, partial cds
3954	16552	29021	0.59	7.2E-02	AW298322.1	EST_HUMAN	UIH-BW0-aj-e-05-0-UI.s1 NCL_CGAP_Sub66 Homo sapiens cDNA clone IMAGE:2732049 3'
4438	17024	29464	3.65	7.2E-02	BF572307.1	EST_HUMAN	602077757F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251950 5'
5223	17788	30207	0.89	7.2E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
5491	18125	30533	2.8	7.2E-02	U67531.1	NT	Methanococcus jennaschii section 73 of 150 of the complete genome
5492	18126	30534	8.6	7.2E-02	P11120	SWISSPROT	CALMODULIN
6265	18873		0.83	7.2E-02	BF217696.1	EST_HUMAN	601883905F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4096224 5'
7220	18751	32607	1.27	7.2E-02	BF216086.1	EST_HUMAN	601883558F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095710 5'
7261	19789		1.54	7.2E-02	5834897	NT	Strongylocentrotus purpuratus mitochondrion, complete genome
8128	20669	33578	0.69	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8128	20669	33579	0.69	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8994	21532		0.5	7.2E-02	Y17217.1	NT	Lactococcus lactis cspe gene
9495	21985		0.57	7.2E-02	X16349.1	NT	Human gene for sex hormone-binding globulin (SHBG)
9529	22028	34988	2.28	7.2E-02	AV712452.1	EST_HUMAN	AV712452 DCA Homo sapiens cDNA clone DCAUG01 5'
9674	22173	35149	4.69	7.2E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
9828	22326	35307	1.01	7.2E-02	BF125399.1	EST_HUMAN	601763523F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026436 5'
9914	22410	35366	2.73	7.2E-02	AW873187.1	EST_HUMAN	hq24111.x1 NCL_CGAP_Ad11 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q9Z340 Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN. ;

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10254	22749	35737	2.11	7.2E-02	U82695.2	NT	Homo sapiens zinc finger protein 82 (ZFP82), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
10370	22864	35857	5.88	7.2E-02	BE565003.1	EST_HUMAN	601343926F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685651 5'
10392	22866		3.22	7.2E-02	BE539214.1	EST_HUMAN	601065194F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451559 5'
10782	23315	36324	6.18	7.2E-02	AF049874.1	NT	Rattus norvegicus bHLH transcription factor Mist1 (Mist1) gene, complete cds
11822	24182	31033	1.54	7.2E-02	AA773696.1	EST_HUMAN	af81a04.11 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1048398 5'
11857	24216		4.88	7.2E-02	AJ230796.1	EST_HUMAN	AJ230796 Homo sapiens library (Seranski P) Homo sapiens cDNA clone PS13DS 3'
11814	24252		2.01	7.2E-02	AA584465.1	EST_HUMAN	nc05h08.s1 NCI_CGAP_Phet1 Homo sapiens cDNA clone IMAGE:1099839 3'
11979	24280		3.59	7.2E-02	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
11885	24858		7.52	7.2E-02	AW900962.1	EST_HUMAN	CM4-NN1009-200300-116-c11 NN1009 Homo sapiens cDNA
12514	24633		1.65	7.2E-02	AA401779.1	EST_HUMAN	z57c12.11 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726454 5'
1948	14532	27088	1.42	7.1E-02	L02290.1	NT	Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds
2331	14802	27473	4.53	7.1E-02	BF208802.1	EST_HUMAN	601872281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4092981 5'
7848	20390	33282	0.84	7.1E-02	AI125284.1	EST_HUMAN	q02a10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736922 3'
11700	24113		6.04	7.1E-02	BE304764.1	EST_HUMAN	601143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5'
554	13185	25663	0.97	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1547	14139		1.43	7.0E-02	X66677.1	NT	Martella Mcut-1 gene
1798	14386	26933	0.94	7.0E-02	AA056343.1	EST_HUMAN	z66f04.s1 Strategene colon (#937204) Homo sapiens cDNA clone IMAGE:509599 3'
3064	15680	28153	2.03	7.0E-02	AW138152.1	EST_HUMAN	UI-H-B11-acy-c-07-UJ.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'
3866	16564	29033	1.71	7.0E-02	AA815438.1	EST_HUMAN	af65a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375678 3' similar to gb:K03002 60S
4118	18712	29168	1.11	7.0E-02	BE070284.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN);
4219	18807		1.11	7.0E-02	AW792962.1	EST_HUMAN	QV4-BT0407-280100-080-e10 BT0407 Homo sapiens cDNA
4284	16880	28327	1.28	7.0E-02	AF077821.1	NT	CM0-UJ0001-060300-270-e12 UJ0001 Homo sapiens cDNA
5063	17636	30079	9.56	7.0E-02	BF381987.1	EST_HUMAN	Canis familiaris inducible nitric oxide synthase mRNA, complete cds
5590	18211		0.84	7.0E-02	Y09143.2	NT	601816291F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050071 5'
7431	18655	32820	0.88	7.0E-02	AV689285.1	EST_HUMAN	Lumbricus rubellus mRNA for cyclophilin B
9027	21564	34493	1.41	7.0E-02	9628113	NT	AV689285 GKC Homo sapiens cDNA clone GKCAE06 5'
9515	22015	34973	1.25	7.0E-02	K02901.1	NT	African swine fever virus, complete genome
8863	22360	35340	0.73	7.0E-02	U27266.1	NT	Rat Ig germline epsilon H-chain gene C-region, 3' end
11251	23781	36837	2.68	7.0E-02	AA724285.1	EST_HUMAN	Human myosin binding protein H (MyBP-H) gene, complete cds
							Human myosin binding protein H (MyBP-H) gene, complete cds
							TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
540	13171	25649	11.84	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
540	13171	25650	11.84	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1378	13971		1.34	6.9E-02	4507968	NT	Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products
3860	16458	28921	1.16	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
3860	16458	28922	1.16	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
							Enterococcus faecium cysteine aminopeptidase (pepC) gene, partial cds; phospho-beta-glucosidase BglB (bglB), beta-glucosidase specific transport protein (bglS), transcription antiterminator (bglR), enterocin B precursor (entB), enterocin B immunity protease
5381	17940	30354	3.58	6.9E-02	AF121254.1	NT	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds
7998	20338		1.13	6.9E-02	U12022.1	NT	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds
8488	21027	33944	1.1	6.9E-02	BE567435.1	EST_HUMAN	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
8488	21027	33945	1.1	6.9E-02	BE567435.1	EST_HUMAN	601340661F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
9048	21585	34516	0.81	6.9E-02	U22987.1	NT	Barbarie duck parvovirus REP protein (rep) and three capsid protein VP (vp) genes, complete cds
11853	24213		17.81	6.9E-02	X74315.1	NT	X.laevus XFD2 mRNA for fork head protein
12031	24321		1.96	6.9E-02	P44621	SWISSPROT	PROTEIN TRANSPORT PROTEIN HOF6 HOMOLOG
12258	24468		3.68	6.9E-02	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
1926	14511	27065	1.83	6.8E-02	AA496759.1	EST_HUMAN	ae30702.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1926	14511	27066	1.83	6.8E-02	AA496759.1	EST_HUMAN	ae30702.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1950	14534	27090	3.99	6.8E-02	AF156673.1	NT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
2023	14605	27170	1.88	6.8E-02	BE263781.1	EST_HUMAN	Homo sapiens putative hepatic transcription factor (WBSCR14) gene, complete cds
4651	17233		0.66	6.8E-02	BE141076.1	EST_HUMAN	601194141F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537708 5'
6980	19478		4.63	6.8E-02	BE061890.1	EST_HUMAN	MR0-HT0069-071099-001-c05 HT0069 Homo sapiens cDNA
7324	19851	32713	8.08	6.8E-02	AL163268.2	NT	RC1-BT0254-090300-017-009 BT0254 Homo sapiens cDNA
8230	20771	33690	5.36	6.8E-02	AJ248287.1	NT	Homo sapiens chromosome 21 segment HS21C088
8230	20771	33691	5.36	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
11846	25064		2.48	6.8E-02	T03214.1	EST_HUMAN	Pyrococcus abyssi complete genome; segment 5/6
11783	24168		2.42	6.8E-02	AA758014.1	EST_HUMAN	FB4A8 Fetal brain, Stragene Homo sapiens cDNA clone FB4A8 3' end similar to LINE-1
12360	24547		1.37	6.8E-02	AW975839.1	EST_HUMAN	ah67705.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320705 3'
12444	24580		2.87	6.8E-02		NT	EST1387948 IMAGE resequences, MAGN Homo sapiens cDNA
12650	25008	30614	1.54	6.8E-02		NT	Mus musculus latent TGF beta binding protein (Tgfb), mRNA
1576	14169		1.51	6.7E-02	AF115636.1	NT	Rattus norvegicus Growth factor independent-1 (Gfi1), mRNA
1938	14522	27078	3.82	6.7E-02	AJ220285.1	EST_HUMAN	Oncorhynchus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP1*01 allele, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3780	16380	28844	4.61	6.7E-02	P17278	SWISSPROT	HOMEOBOX PROTEIN HOX-D4 (HOXA)
4842	17420	29873	3.51	6.7E-02	AF001514.1	NT	Bacillus halodurans genomic DNA, section 8/14
7792	20335	33241	0.63	6.7E-02	X62895.1	NT	H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)
7792	20335	33242	0.63	6.7E-02	X62895.1	NT	H.sapiens DNA for cGMP phosphodiesterase (exons 4-22)
9518	22018	34975	0.75	6.7E-02	AW137359.1	EST_HUMAN	UI-H-B11-acr-g-01-Q.U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
9518	22018	34976	0.75	6.7E-02	AW137359.1	EST_HUMAN	UI-H-B11-acr-g-01-Q.U1.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
2225	14800	27372	3	6.6E-02	AJ289241.1	NT	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
3510	16115	28594	9.7	6.6E-02	R64306.1	EST_HUMAN	Y18b10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139578 3'
3524	16129	28609	3.24	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3524	16129	28610	3.24	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
4154	16746	29200	1.83	6.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
5114	17686	30122	11.2	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5114	17686	30123	11.2	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5184	17733	30160	0.57	6.6E-02	AA393244.1	EST_HUMAN	z74a07.r1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:728052 5' similar to gb:L04270 TUMOR
5164	17733	30161	0.57	6.6E-02	AA393244.1	EST_HUMAN	NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);
6698	19294	32099	4.11	6.6E-02	X06411.1	NT	z74a07.r1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:728052 5' similar to gb:L04270 TUMOR
7888	20430	33339	1.58	6.6E-02	AF052572.1	NT	NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);
8409	20949	33869	0.72	6.6E-02	AF060655.1	NT	P.vulgaris mRNA for chalcone synthase
8714	21253	34312	0.49	6.6E-02	O60673	SWISSPROT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
8852	21391	34313	0.52	6.6E-02	9829198	NT	Dictyostelium discoideum darlin (darA) gene, complete cds
8852	21391	34313	0.52	6.6E-02	9829198	NT	DNA POLYMERASE ZETA CATALYTIC SUBUNIT (HREV3)
9862	22359	35339	0.58	6.6E-02	AI488752.1	EST_HUMAN	Human respiratory syncytial virus, complete genome
9899	22494	35483	1.54	6.6E-02	Y07848.1	NT	Human respiratory syncytial virus, complete genome
10029	22524	36379	0.53	6.6E-02	11430559	NT	Homo sapiens EWS, gar22, rrp22 and bam22 genes
10842	23363	36379	7.09	6.6E-02	BF374248.1	EST_HUMAN	Homo sapiens vinculin (VCL), mRNA
12251	24462		2.87	6.6E-02	9837891	NT	MR1-SN0064-010600-006-a12 SN0064 Homo sapiens cDNA
12585	24678		1.36	6.6E-02	AF167430.1	NT	Mus musculus DJPB gene (Djpb), mRNA
608	13236	25710	1.65	6.6E-02	BF027639.1	EST_HUMAN	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region
1024	13635	26151	2.61	6.6E-02	U47624.1	NT	601671046f1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954178 5'
1435	14028	26568	3.4	6.6E-02	U47624.1	NT	Homo sapiens E2F-like protein (LOC51270), mRNA
1770	14360	26905	1.42	6.6E-02	AE000784.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
5349	17809	30324	0.88	6.6E-02	D45898.1	NT	Aquifex apiculatus section 86 of 108 of the complete genome
							Caenorhabditis elegans DNA for ryanodine receptor, complete cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5747	18373	31081	1.79	6.5E-02	AA443991.1	EST_HUMAN	z448h12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:756743 3' similar to gb:M26038
6664	19260	32064	0.89	6.5E-02	BF685340.1	EST_HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN);
7051	18070	30461	0.86	6.5E-02	U22661.1	NT	602118887F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276029 5'
9854	22352	35332	0.65	6.5E-02	BE963200.2	EST_HUMAN	Azotobacter vinelandii ATCC 9046 negative regulator MucB (mucB) gene, partial cds
9854	22352	35332	0.65	6.5E-02	BE963200.2	EST_HUMAN	601656817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865837 3'
10363	22857	35949	0.59	6.5E-02	BF106300.1	EST_HUMAN	601656817R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3865837 3'
10518	23056	36067	5.88	6.5E-02	AA195648.1	EST_HUMAN	601823511F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4043138 5'
11869	24091		5.28	6.5E-02	M21496.1	NT	z332p05.s1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:665144 3'
12040	24327		3.84	6.5E-02	AF102993.1	NT	Rabbit microsomal epoxide hydrolase
601	13230	25703	1.74	6.4E-02	X94549.1	NT	Nectria haematococca kinsin related protein 2 (KRP2) gene, complete cds
5841	18270	30743	1.21	6.4E-02	AI191956.1	EST_HUMAN	A. carterae precursor of peridinin-chlorophylla-protein (PCP) gene
6261	18869	31639	5.4	6.4E-02	AF052733.1	NT	qeo7b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR8.b3
6261	18869	31640	5.4	6.4E-02	AF052733.1	NT	LTR8 repetitive element;
6534	19134	31927	0.88	6.4E-02	AI672896.1	EST_HUMAN	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6907	19641	32477	4.7	6.4E-02	BE974448.1	EST_HUMAN	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
8278	20819		2.66	6.4E-02	6753323	NT	we73g12.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346790 3'
8599	21138	34052	3.59	6.4E-02	AA093305.1	EST_HUMAN	601680425R2 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:3950503 3'
9055	21592	34522	0.85	6.4E-02	AF150195.1	EST_HUMAN	Mus musculus chaperonin subunit 6a (zeta) (Cct6a), mRNA
9506	22006		0.81	6.4E-02	BE834083.1	EST_HUMAN	k1419.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9633	22133	35098	1.79	6.4E-02	AB011126.1	NT	AF150195 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAIA10
10162	22657	35652	0.68	6.4E-02	AF087150.1	NT	RC1-OT0083-150600-014-g06 OT0083 Homo sapiens cDNA
10162	22657	35653	0.68	6.4E-02	AF087150.1	NT	Homo sapiens mRNA for KIAA0554 protein, partial cds
							Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
							Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
							Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds
11554	24002	37074	2.05	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds
11554	24002	37075	2.05	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds
11831	24971		4.86	6.4E-02	AF107890.1	NT	Homo sapiens mucin 5B (MUC5B) gene, partial cds
11866	24296	30893	2.86	6.4E-02	AJ277174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1791	14381	26928	3.03	6.3E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, Muts homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
3684	18266		2.41	6.3E-02	P37092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
6285	18893	31682	1.1	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
7291	18819		1.05	6.3E-02	X97869.1	NT	H. sapiens gene encoding La autoantigen
9215	21732	34675	0.96	6.3E-02	AJ243916.1	NT	Drosophila melanogaster Dornin gene, exons 1-3
9927	22423	35397	2.86	6.3E-02	AB010162.1	NT	Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: CMR-152
10172	22667		0.97	6.3E-02	AV698070.1	EST_HUMAN	AV698070 GKC Homo sapiens cDNA clone GKCAHE01 5'
10594	18893	31662	3.6	6.3E-02	BF210736.1	EST_HUMAN	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
4337	16924	29365	3.3	6.2E-02	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
4431	17017		1.04	6.2E-02	AF271235.1	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4882	17264		6.75	6.2E-02	O62191	SWISSPROT	52 KD RO PROTEIN (SJOJREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52)
6889	19624	32459	0.75	6.2E-02	D49530.1	NT	Spirulina platensis DNA for adenylate cyclase, complete cds
7623	20136	33014	0.78	6.2E-02	U41453.1	NT	Rattus norvegicus PKC binding protein and substrate mRNA, complete cds
8877	25123	34742	0.81	6.2E-02	M61101.1	NT	Porcine group C rotavirus (strain Cowden) outer membrane protein (VP7) mRNA, complete cds
9267	21783	34742	0.5	6.2E-02	AA778450.1	EST_HUMAN	af20a06 s1 Soares_total_fetus_Nb2Hf8_9w Homo sapiens cDNA clone IMAGE:1032178 3'
9401	21910	34859	1.05	6.2E-02	6677868	NT	Mus musculus stromal cell derived factor receptor 2 (Sdfr2), mRNA
11027	23541	36576	1.74	6.2E-02	AF217480.1	NT	Homo sapiens fragile 16D oddo reductase (FOR) gene, exons 8, 9, and partial cds
11228	23757	36914	1.89	6.2E-02	AJ242735.1	NT	Metarhizium anisopliae mRNA for Chymotrypsin (chy1) gene
11770	25097		8.34	6.2E-02	AE000750.1	NT	Aquifex aeolicus section 82 of 109 of the complete genome
12200	24426	30851	3.56	6.2E-02	BF112039.1	EST_HUMAN	7137h08.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523815 3' similar to
277	12834	25420	4.8	6.1E-02	D18471.1	NT	Human mRNA, Xq terminal portion
4063	16660		2.78	6.1E-02	U73325.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AKK1) gene, complete cds
4759	17340	29786	1.09	6.1E-02	AF118413.1	NT	Lupinus albus 1-aminocyclopropane-1-carboxylate synthase 3 (ACS3) gene, complete cds
4759	17340	29787	1.09	6.1E-02	AF118413.1	NT	Lupinus albus 1-aminocyclopropane-1-carboxylate synthase 3 (ACS3) gene, complete cds
6262	18670		1.42	6.1E-02	4507070	NT	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
8207	20748	33661	3.31	6.1E-02	X99288.1	NT	H. sapiens mRNA for B-HLH DNA binding protein
8595	21134	34048	0.95	6.1E-02	BE071853.1	EST_HUMAN	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934804 3'
8595	21134	34049	0.95	6.1E-02	BE071853.1	EST_HUMAN	601651086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934804 3'
10608	23142	36153	6.34	6.1E-02	BE179543.1	EST_HUMAN	IL3-HT0618-110500-138-C06 HT0618 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11726	25009		23.38	6.1E-02	X70988.1	NT	S Japonicum mRNA for serine-enzyme
12317	24880		1.39	6.1E-02	AI886611.1	EST_HUMAN	ts59107.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2292901 3'
12464	24592		7.98	6.1E-02	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
1305	13899	28419	1.01	6.0E-02	AE001777.1	NT	Thermotoga maritima section 89 of 136 of the complete genome
2700	15257	27825	1.15	6.0E-02	AW968848.1	EST_HUMAN	EST380924 IMAGE resequences: MAGJ Homo sapiens cDNA
2801	15353		1.58	6.0E-02	AB031289.1	NT	Mesocostoides cord mitochondria DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
2983	12777	25259	1.09	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
2983	12777	25260	1.09	6.0E-02	AA188730.1	EST_HUMAN	zp78c04.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
3266	15878	28360	1.24	6.0E-02	AA372376.1	EST_HUMAN	EST84266 Cdon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3266	15878	28361	1.24	6.0E-02	AA372376.1	EST_HUMAN	EST84266 Cdon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3697	16298		1.01	6.0E-02	BE964443.2	EST_HUMAN	601658150R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876060 3'
5104	17676	30116	0.95	6.0E-02	Z67739.2	NT	Streptococcus pneumoniae parC, parE and transposase genes and ORF DNA
5595	18225		1.99	6.0E-02	AW370211.1	EST_HUMAN	RC3-810253-011199-013-504 BT0253 Homo sapiens cDNA
6384	18988	31746	1.43	6.0E-02	AI807537.1	EST_HUMAN	wf48h05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358873 3' similar to contains L1.11 L1.1 repetitive element
7063	18082	30438	2.73	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7063	18082	30439	2.73	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7239	19768	32624	2.17	6.0E-02	BF382349.1	EST_HUMAN	601815274F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4049226 5'
7672	20184	33072	1.94	6.0E-02	AI204275.1	EST_HUMAN	qf58b08.x1 Soares_testis NIH_T Homo sapiens cDNA clone IMAGE:1754189 3'
8361	20901		0.57	6.0E-02	11488495	NT	Reclinomonas americana mitochondrion, complete genome
9196	21713	34656	1.12	6.0E-02	AI623167.1	EST_HUMAN	ts78a06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2237362 3'
9196	21713	34657	1.12	6.0E-02	AI623167.1	EST_HUMAN	ts78a06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2237362 3'
9327	21841	34792	2	6.0E-02	AJ245365.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
9327	21841	34793	2	6.0E-02	AJ245365.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
9819	22317	35299	0.51	6.0E-02	AA309797.1	EST_HUMAN	EST180664 Jurkat T-cells V Homo sapiens cDNA 5' end similar to heat shock protein 1, 60 kDa-like
9819	22317	35300	0.51	6.0E-02	AA309797.1	EST_HUMAN	EST180664 Jurkat T-cells V Homo sapiens cDNA 5' end similar to heat shock protein 1, 60 kDa-like
11214	23717		2.13	6.0E-02	AA128386.1	EST_HUMAN	zn87c08.r1 Stratagene lung carcinoma 957218 Homo sapiens cDNA clone IMAGE:565166 5' similar to gb:X69181.60S RIBOSOMAL PROTEIN L31 (HUMAN);
11985	24295	30982	1.43	6.0E-02	11431702	NT	Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2), mRNA
12394	24554		6.04	6.0E-02	AI809273.1	EST_HUMAN	wf69h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR:O60298 O60298 KIAA0551 PROTEIN;

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
250	12910	25393	4.76	5.9E-02	AW934719.1	EST_HUMAN	RC1-DT0001:290100-012-e10 DT0001 Homo sapiens cDNA
3012	15028	28107	2.75	5.9E-02	AF190289.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
4768	17349	29798	0.97	5.9E-02	AL161535.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
4768	17349	29800	0.97	5.9E-02	AL161535.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
4852	17430		0.6	5.9E-02	AF166111.1	NT	Duck parvovirus strain 90-2183 capsid protein (VP3) gene, partial cds
4996	17570	30014	0.96	5.9E-02	AF006304.1	NT	Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
6873	24774	32374	0.87	5.9E-02	AF145880.1	NT	Drosophila melanogaster LD23107 sting (sting) mRNA, complete cds
8552	21081	34011	1.99	5.9E-02	9055249	NT	Mus musculus inroquid related homebox 5 (Drosophila) (Inr5), mRNA
8372	20311		0.82	5.9E-02	BF242748.1	EST_HUMAN	601877609F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105994 5'
10664	23186		3.41	5.9E-02	8679870	NT	Mus musculus follistatin-like (Fst), mRNA
10898	23419	38438	2.35	5.9E-02	11433356	NT	Homo sapiens ninein (LOC51199), mRNA
11429	23880		1.83	5.9E-02	AJ240733.1	NT	Gallus gallus HKC9 telomere junction
968	13579		5.2	5.9E-02	D90110.1	NT	Thiobacillus ferrooxidans merC, merA genes and URF-1
1700	14293	26828	1	5.9E-02	Q61768	SWISSPROT	KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC)
2886	15504		0.98	5.9E-02	AJ223621.1	NT	Populus trichocarpa CCoAOMT1 gene, exon 1 to exon 5
3725	16326	28793	1.35	5.9E-02	AE001775.1	NT	Thermotoga maritima section 87 of 136 of the complete genome
4446	17032	29473	5.29	5.9E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4446	17032	29474	5.29	5.9E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4845	17227	29682	5.04	5.9E-02	AI247505.1	EST_HUMAN	q156f01.x1 Soares_fetal_liver_spleen_1NPLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:MT13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4845	17227	29683	5.04	5.9E-02	AI247505.1	EST_HUMAN	q156f01.x1 Soares_fetal_liver_spleen_1NPLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to gb:MT13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4874	17256		1.98	5.9E-02	AF086264.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
5284	17656	30282	0.57	5.9E-02	AF275366.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
5284	17656	30283	0.57	5.9E-02	AF275366.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
6068	18085	31428	1.52	5.9E-02	AA190894.1	EST_HUMAN	zp86a11.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:927068 3'
7670	20182	33069	2.73	5.9E-02	M99150.1	NT	Human polymorphic microsatellite DNA
7670	20182	33070	2.73	5.9E-02	M99150.1	NT	Human polymorphic microsatellite DNA
8601	21140	34054	0.76	5.9E-02	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
11871	24223		2.86	5.9E-02	AF220177.1	NT	Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds
12177	25085		6.45	5.9E-02	AA604269.1	EST_HUMAN	no75611.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112684 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3093	15708	28179	1.13	5.7E-02	AI081644.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
3107	15722	28193	1.6	5.7E-02	AF119117.1	NT	CE08611 ; Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
3769	16370		0.96	5.7E-02	AF001292.1	NT	Chironomus thummi thummi globin VIIA.1 (ctt-7A.1), globin 9.1 (ctt-9.1), globin II-beta (ctt-2beta), non-functional globin XIII (ctt-13RT), globin XII (ctt-12) and globin XI (ctt-11) genes, complete cds
3871	16469	28932	2.44	5.7E-02	AW986791.1	EST_HUMAN	EST378865 MAGI resequences, MAGI Homo sapiens cDNA
4795	17373		1.06	5.7E-02	M95098.1	NT	Bos laurus lysozyme gene (cow 3), complete cds
5334	17895	30310	0.99	5.7E-02	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
6039	18658		0.8	5.7E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8098	20637	33548	1.46	5.7E-02	AJ296090.1	NT	Rattus norvegicus mRNA for potassium channel, alpha subunit (kv2.2 gene)
9764	22282	35245	0.65	5.7E-02	6681260	NT	Mus musculus ec2 oncogene (Ec2), mRNA
11067	23579	36617	4.17	5.7E-02	AJ752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
11067	23579	36618	4.17	5.7E-02	AJ752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
11227	23758		1.56	5.7E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
12085	24891		12.96	5.7E-02	D50320.1	NT	Pig DNA for SPAL-2, complete cds
12257	24467		1.71	5.7E-02	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
12334	24865		3.31	5.7E-02	AF217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
12483	25074		8.94	5.7E-02	AF261280.1	NT	Pen troglodytes apolipoprotein-E gene, complete cds
12622	24700	30863	1.58	5.7E-02	R48513.1	EST_HUMAN	yf64d10.s1 Scores breast 2NtHBst Homo sapiens cDNA clone IMAGE:153523 3' similar to contains L1 repetitive element ;
1574	14167	26698	1.2	5.6E-02	AF094455.1	NT	Hydrocotyle rotundifolia ribosomal protein L16 (rp16) gene, intron; chloroplast gene for chloroplast product
4746	17327	29769	1.21	5.6E-02	AB013100.1	NT	Lycopodium obscurum LE-ACS6 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
4808	17384	29834	1.2	5.6E-02	AA290599.1	EST_HUMAN	zs45c01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700476 3'
6766	19359	32168	5.98	5.6E-02	AW172708.1	EST_HUMAN	xp02c10.x1 NCI_CGAP_U22 Homo sapiens cDNA clone IMAGE:2656030 3' similar to TR:Q94978 O94979 KIAA0905 PROTEIN ;
6971	19548	32372	0.9	5.6E-02	AA866182.1	EST_HUMAN	cd47f12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371119 3' similar to contains Alu repetitive element; contains element L1 repetitive element ;
7205	19736	32589	3.1	5.6E-02	BE080001.1	EST_HUMAN	QV0-BN0147-230400-214-g07 BN0147 Homo sapiens cDNA
8737	21276	34198	2.2	5.6E-02	BE542663.1	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'
8737	21276	34199	2.2	5.6E-02	BE542663.1	EST_HUMAN	601067158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9726	22224	35201	1.07	5.6E-02	AA482864.1	EST_HUMAN	m148407.s1 NCL_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:923245 similar to TR:G768859 G768859 LAMINA ASSOCIATED POLYPEPTIDE 1C.
11439	23889		2.33	5.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
2679	15237	27804	6.14	5.5E-02	X97869.1	NT	H. sapiens gene encoding La autoantigen
3251	15863	28345	3.83	5.5E-02	6755501	NT	Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA
4298	18882	28328	1.12	5.5E-02	L41561.1	NT	Galid herpesvirus mRNA fragment
5840	18464	31188	3.19	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
6178	18464	31188	3.86	5.5E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
7412	19937	32802	1.77	5.5E-02	6755902	NT	Mus musculus tufellin 1 (Tuf1), mRNA
8063	20605	33516	0.77	5.5E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1), mRNA, complete cds
8063	20605	33517	0.77	5.5E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1), mRNA, complete cds
9573	22073	35034	0.61	5.5E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
9573	22073	35035	0.61	5.5E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
9664	22163	35136	1.28	5.5E-02	U69492.1	NT	Mus musculus second IL1 receptor alpha chain (IL1Ra2) gene, exons 1 and 2
10898	23418	36435	11.52	5.5E-02	U09771.1	NT	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhaK), glycerol dehydrogenase (dhaD), transcriptional activator (dhaR), 1,3-propanediol dehydrogenase (dhaT), glycerol dehydratase (dhaB), >
3054	15670		0.85	5.4E-02	AJ277468.1	NT	Oryza sativa ribb3-1 gene for putative Bowman Birk trypsin inhibitor
3469	18013		6.27	5.4E-02	BE073468.1	EST_HUMAN	RC5-BT05559-140200-012-C03 BT05559 Homo sapiens cDNA
3982	16580	28051	0.59	5.4E-02	U85806.1	NT	Hirudo medicinalis SNAP-25 homolog mRNA, complete cds
5119	17691	30128	2.48	5.4E-02	U53528.1	NT	Xenopus laevis homeobox protein (Vox-1) mRNA, complete cds
8067	20609		1.11	5.4E-02	Z99116.1	NT	Bacillus subtilis complete genome (section 13 of 21); from 2395281 to 2613730
9001	21638	34467	0.61	5.4E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
10578	23113	36128	1.89	5.4E-02	U20780.1	NT	Neurospora crassa ubiquitin-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
11058	23570	36606	1.56	5.4E-02	BF371289.1	EST_HUMAN	RC6-FN0112-190700-021-D06 FN0112 Homo sapiens cDNA
11058	23570	36607	1.56	5.4E-02	BF371289.1	EST_HUMAN	RC6-FN0112-190700-021-D06 FN0112 Homo sapiens cDNA
11968	24882		2.9	5.4E-02	U44684.1	NT	Rana catesbeiana heat shock protein 30 (HSP30) mRNA, complete cds
1091	13696	26205	1.59	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1091	13696	26206	1.58	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-a09 ST0213 Homo sapiens cDNA
1553	14145	26879	21.63	5.3E-02	T94759.1	EST_HUMAN	y337f12.1 Stratiogene lung (#337210) Homo sapiens cDNA clone IMAGE:119851 5' similar to gb:K01506
2541	15105	27677	2.71	5.3E-02	AJ276408.1	NT	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN); Pseudomonas putida tgsS gene
2969	15585	28066	0.88	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2669	15585	28067	0.88	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3187	15789	28271	4.52	5.3E-02	AJ276408.1	NT	Pseudomonas putida tlgS gene
5248	17811	30234	0.75	5.3E-02	AB051897.1	NT	Mus musculus Scya6, Scya8, Scya10-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
5250	17813	30236	8.25	5.3E-02	M80463.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds
5522	18154	30568	1.97	5.3E-02	AE000527.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
5522	18154	30569	1.97	5.3E-02	AE000527.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
6251	18860	31632	0.71	5.3E-02	M85289.1	NT	Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds
6864	19541	32363	4.23	5.3E-02	9695413	NT	Lymphocystis disease virus 1, complete genome
7149	19882	32523	1.55	5.3E-02	U32832.1	NT	Haemophilus influenzae Rd section 147 of 163 of the complete genome
7398	19821		2.05	5.3E-02	S78221.1	NT	nuclear protein TIF1 isoform [mice, mRNA, 4053 nt]
7818	20290	33189	0.52	5.3E-02	P38742	SWISSPROT	HYPOTHEICAL 130.0 KD PROTEIN IN SNF6-SPO11 INTERGENIC REGION
8344	20885		0.54	5.3E-02	U10098.1	NT	Mus musculus 129/Sv cystatin C (cst3) gene, complete cds
9053	21590	34521	1.83	5.3E-02	X03127.1	NT	Podospira anserina mitochondrial epsilon-sen DNA
10038	22533	35529	0.54	5.3E-02	AB022605.1	NT	Homo sapiens hCMT1b mRNA for mRNA (guanine-7-methyltransferase, complete cds)
10038	22533	35530	0.54	5.3E-02	AB022605.1	NT	Homo sapiens hCMT1b mRNA for mRNA (guanine-7-methyltransferase, complete cds)
10156	22651		0.62	5.3E-02	Y07807.1	NT	D. rerio mRNA for zp-23 POU gene, splice variant (neurula, 9-16 hpf and postmitogenesis, 20-28 hpf)
10235	22730	35721	0.65	5.3E-02	X68432.1	NT	B. rerio pou3j mRNA for transcription factor
2324	14895		116.52	5.2E-02	5031908	NT	Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA
3148	15762	28228	2.4	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3148	15762	28229	2.4	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
4013	16611	29084	0.7	5.2E-02	AF236101.1	NT	Arabidopsis thaliana putative dicarboxylate diion protein (Crd1) mRNA, complete cds
4365	16952	29392	3.61	5.2E-02	U07132.1	NT	Human steroid hormone receptor Nrr-1 mRNA, complete cds
4846	17424	29877	1.28	5.2E-02	L33246.1	NT	Drosophila melanogaster filament protein homolog (sepi) gene, complete cds
6076	18693	31439	0.89	5.2E-02	U14731.1	NT	Saccharomyces cerevisiae Cdc54p (CDC54) gene, complete cds
6255	18864		1.42	5.2E-02	A830985.1	EST_HUMAN	w80e04.x1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409150 3' similar to contains MER15.b1 MER15 repetitive element ;
7318	19845	32706	1.19	5.2E-02	P38322	SWISSPROT	DNA POLYMERASE PROCESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) (DNA-BINDING GENE 18 PROTEIN)
8136	20877		1.98	5.2E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21G004
9845	22145	35113	1.97	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
9845	22145	35114	1.97	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12224	24445		1.84	5.2E-02	Q03030	SWISSPROT	OXALOACETATE DECARBOXYLASE ALPHA CHAIN
12327	24513		1.27	5.2E-02	D63362.1	NT	Mouse DNA for regII gamma protein, complete cds
2402	14970		1.14	5.1E-02	AL134071.1	EST_HUMAN	DKFZp547D073_1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D073 5'
4282	16868	29315	0.73	5.1E-02	AE001301.1	NT	Chlamydia trachomatis section 28 of 87 of the complete genome
4908	17483	29941	8.03	5.1E-02	AF085167.1	NT	Hordeum vulgare receptor-like kinase ARK1AS gene, partial cds
5205	17770	30193	1.14	5.1E-02	BE957423.2	EST_HUMAN	60165356SR2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3836361 3'
6777	19369	32182	0.76	5.1E-02	AF280369.1	NT	HIV-1 patient 96 from Italy protease (pol) gene, complete cds
6942	18050	30472	1.6	5.1E-02	BF378626.1	EST_HUMAN	QVO-LM0051-250800-350-b08 UM0051 Homo sapiens cDNA
8195	20736	33648	0.82	5.1E-02	M28434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8195	20736	33647	0.82	5.1E-02	M28434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8268	20829	33750	1.48	5.1E-02	AJ131896.1	NT	Spodoptera littoralis mRNA for 3-dehydrodyscine 3beta-reductase
8818	21357	34282	0.63	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
8818	21357	34283	0.63	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (CK 14)
9723	22221	35198	8.16	5.1E-02	AF012898.1	NT	Candida albicans protein phosphatase Sed1 homolog (SSD1) gene, complete cds
10084	22579	35572	1.83	5.1E-02	P40603	SWISSPROT	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
10709	23237	36250	2.86	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
10709	23237	36251	2.88	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
12332	24448		1.51	5.1E-02	AF062467.1	NT	Cucumis melo polygalacturonase precursor (MPG3) mRNA, complete cds
508	13141	25828	1.76	5.0E-02	AF088004.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1246	13843	26360	6.63	5.0E-02	Z69104.1	NT	Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080
2034	14516	27182	3.63	5.0E-02	P02810	SWISSPROT	SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1/PRP-3) (PRP-2/PRP-4) (PIF-FIPF-S) (PROTEIN A PROTEIN C) [CONTAINS: PEPTIDE P-C]
2845	13834	26150	1.78	5.0E-02	U72742.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3381	15890		1.42	5.0E-02	7305610	NT	Mus musculus Unc-51 like kinase 2 (C. elegans) (Ulk2) mRNA
3655	16258		1.06	5.0E-02	U32782.1	NT	Haemophilus influenzae Rd section 97 of 163 of the complete genome
3747	16348	28816	5.6	5.0E-02	U12789.2	NT	Antheraea pernyi period clock protein homolog mRNA, complete cds
5102	17674	30114	1.11	5.0E-02	AF188530.1	NT	Homo sapiens ubiquitously tetrapeptide containing protein RoXan mRNA, partial cds
6278	18887	31856	0.74	5.0E-02	AF086284.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
6450	19051		1.23	5.0E-02	AJ242625.1	NT	Mus musculus Dmp-1 gene, exons 1-6
7544	20064	32838	10.74	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
10101	22596	35589	1.13	5.0E-02	AF305238.1	NT	Mus musculus Fas-interacting serine/threonine kinase 3 (Fas3) mRNA, complete cds
11364	23816	36877	2.87	5.0E-02	U67600.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
11738	24924		7.22	5.0E-02	Q04047	SWISSPROT	NO-ON-TRANSIENT A PROTEIN
242	12901		23.23	4.9E-02	M14230.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
392	13038	25528	3.62	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
392	13038	25529	3.62	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
3328	15938	28414	1.58	4.9E-02	P54258	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLYSIAN ATROPHY PROTEIN)
3628	18231		0.63	4.9E-02	AA188940.1	EST_HUMAN	z48a12.s1 Stralagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632926 3' similar to contains Alu repetitive element, contains element MSR1 repetitive element ;
3651	18254	28726	0.91	4.9E-02	AA400914.1	EST_HUMAN	z78a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
3651	18254	28727	0.91	4.9E-02	AA400914.1	EST_HUMAN	z78a03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
4966	17540	29982	1.59	4.9E-02	AW167821.1	EST_HUMAN	xq56g10.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'
4968	17540	29983	1.59	4.9E-02	AW167821.1	EST_HUMAN	xq56g10.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'
5372	17931	30345	0.81	4.9E-02	7662816	NT	Homo sapiens PRO1848 protein (PRO1848), mRNA
5406	17984		0.91	4.9E-02	AF135416.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
5425	17982		0.98	4.9E-02	AE001774.1	NT	Thermoloba maritima section 86 of 136 of the complete genome
5437	17992	30398	1.03	4.9E-02	M94083.1	NT	Brucella ovis heat shock protein hsp70 (dnaK) gene, complete cds; heat shock protein hsp40 (dnaJ) gene, complete cds
5573	18204	30654	1.95	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
5573	18204	30655	1.95	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
7196	18727	32578	0.99	4.9E-02	AE000980.1	NT	Archaeoglobus fulgidus section 127 of 172 of the complete genome
8551	21090		0.88	4.9E-02	AE002309.1	NT	Chlamydia muridarum, section 40 of 85 of the complete genome
8989	21228	34149	0.7	4.9E-02	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
10193	22688	35681	0.54	4.9E-02	P19532	SWISSPROT	TRANSCRIPTION FACTOR E3
11280	23733	36786	3.67	4.9E-02	AF008303.1	NT	Homo sapiens prepro placental TGF-beta gene, complete cds
12148	24391		1.44	4.9E-02	8923860	NT	Homo sapiens CS box-containing WD protein (LOC55884), mRNA
12431	24573		2.92	4.9E-02	M18394.1	NT	Human gamma-B-crystallin (gamma 1:2) and gamma-C-crystallin (gamma 2:1) genes, complete cds
352	13002	25487	1.15	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
353	13002	25487	1.87	4.8E-02	D16471.1	NT	Human mRNA, Xq terminal portion
514	13147	25631	9.43	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2312	14884	27459	1.96	4.8E-02	W51883.1	EST_HUMAN	z49b02.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325611 3' similar to gb:M30938 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN);
3244	15856	28339	2.34	4.8E-02	X17144.1	NT	Tetrahymena rostrata histone H3II and histone H4II intergenic DNA
4778	17359		1.32	4.8E-02	Z54290.1	NT	S. scrofa gene for skeletal muscle ryanodine receptor
5309	17871	30293	0.87	4.8E-02	U91914.1	NT	Streptococcus constellatus D-alanine:D-alanine ligase gene, partial cds
5380	17939	30352	4.1	4.8E-02	AF198339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
5380	17939	30353	4.1	4.8E-02	AF198339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8080	20622	33535	1.42	4.8E-02	AW398497.1	EST_HUMAN	MR2-ST0129-221099-012-b02 ST0129 Homo sapiens cDNA
9057	21594	34524	1.3	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
9057	21594	34525	1.3	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
12018	24315		1.93	4.8E-02	9632863	NT	Streptococcus thermophilus bacteriophage Sf10, complete genome
6918	19577	32408					ye97109.r1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:281017 5' similar to contains Alu repetitive element
6965	19542	32364	2.98	4.7E-02	W01153.1	EST_HUMAN	
6965	19542	32364	0.78	4.7E-02	BF686625.1	EST_HUMAN	602143554F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304772 5'
6965	19542	32365	0.78	4.7E-02	BF686625.1	EST_HUMAN	602143554F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304772 5'
6998	19498	32317	1.57	4.7E-02	M62752.1	NT	Rat statin-related protein (s1) gene, complete CDS
8193	20734	33644	8.55	4.7E-02	X15543.1	NT	B. taurus mRNA for RE-38-DNA-binding protein
8883	21421	34346	1.12	4.7E-02	X89211.1	NT	H sapiens DNA for endogenous retroviral like element
8906	21444		2.29	4.7E-02	AB026678.1	NT	Gallus gallus Wpki-8 gene, complete cds
8154	21689	34633	6.91	4.7E-02	X15543.1	NT	B. taurus mRNA for RE-36-DNA-binding protein
9565	22065	35024	0.55	4.7E-02	BF305237.1	EST_HUMAN	601892892F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138414 5'
9650	22149		0.55	4.7E-02	A1873042.1	EST_HUMAN	we79c10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347314 3'
10634	23166	36177	1.55	4.7E-02	6754565	NT	Mus musculus ligand of numb-protein X (Lnx), mRNA
11430	23881	36945	1.69	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
11430	23881	36946	1.69	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
11951	25087		6.94	4.7E-02	AV648521.1	EST_HUMAN	AV648521 GLC Homo sapiens cDNA clone GLCBKD02 3'
12322	25089		1.47	4.7E-02	P52951	SWISSPROT	HOMEBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEBOX PROTEIN 2)
292	12948	25435	0.81	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
769	13388	25887	2.44	4.6E-02	AE000445.1	NT	Escherichia coli K-12 MG1655 section 335 of 400 of the complete genome
1335	13929		1.37	4.6E-02	A1014255.1	EST_HUMAN	am50d02.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538978 3' similar to TR:P90533
1403	13996	28525	9	4.6E-02	AV727059.1	EST_HUMAN	P90533 LIMA ; contains element LTR1 repetitive element ;
2530	15094	27696	2.77	4.6E-02	AW236023.1	EST_HUMAN	AV727059 HTC Homo sapiens cDNA clone HTCBW C01 5'
2834	12948	25435	1.83	4.6E-02	BE153583.1	EST_HUMAN	xn24f03.x1 NCL_OGAP_Kid11 Homo sapiens cDNA clone IMAGE:2894853 3' similar to SW:GRF1_HUMAN Q12849 G-RICH SEQUENCE FACTOR-1 ;
3042	15658	28138	0.7	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
3543	15658	28138	0.95	4.6E-02	BE153583.1	EST_HUMAN	PMO-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
4201	16790		0.97	4.6E-02	AF220365.1	NT	Mus musculus nuclear RNA helicase [l/Gu (dix21) gene, complete cds
5909	18531	31256	1.44	4.6E-02	AF076962.1	NT	Haplochromis burtoni gonadotropin-releasing hormone and GnRH-associated peptide precursor (GnRH2) gene, complete cds
6377	18981	31760	3.77	4.6E-02	X61624.1	NT	C.reinhardtii atp2 (atbB) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6377	18981	31761	3.77	4.6E-02	X61824.1	NT	C.reinhardtii alp2 (alpB) mRNA
6891	19625	32481	1.39	4.6E-02	AI149574.1	EST_HUMAN	cd30b06.x1 Soares_placenta_8tc6weeks_2NHP809W Homo sapiens cDNA clone IMAGE:1713971 3'
8590	21129	34046	2.82	4.6E-02	BE154006.1	EST_HUMAN	similar to contains L1.13 L1 repetitive element
11281	23734	36789	4.26	4.6E-02	AA913328.1	EST_HUMAN	PMO-HT0339-060400-009-G12 HT0339 Homo sapiens cDNA
12541	24651		2.54	4.6E-02	X57808.1	NT	q27h09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737 3'
472	13105	25588	2.71	4.5E-02	P22448	SWISSPROT	Human germline immunoglobulin lambda light chain gene
1260	13857	26373	0.78	4.5E-02	AF005730.1	NT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1260	13857	26373	0.78	4.5E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozzlin VP35 gene, complete cds
1840	14428	26980	3.54	4.5E-02	P32182	SWISSPROT	Marburg virus strain M/S.Africa/Johannesburg/1975/Ozzlin VP35 gene, complete cds
2156	14733	27306	3.65	4.5E-02	AE003984.1	NT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
3786	16366	28852	3.84	4.5E-02	AL163278.2	NT	Xyella fastidiosa, section 110 of 229 of the complete genome
6378	18982	31762	1.88	4.5E-02	AJ400877.1	NT	Homo sapiens chromosome 21 segment HS21C078
6631	19227	32032	0.89	4.5E-02	AL163280.2	NT	Homo sapiens ASCJ.3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
8332	20873	33795	1.8	4.5E-02	AF036694.1	NT	Homo sapiens chromosome 21 segment HS21C080
9860	22357	35337	5.91	4.5E-02	AA325216.1	EST_HUMAN	Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds
10117	22612	35602	0.77	4.5E-02	AB000470.1	NT	EST28167 Cerebellum II Homo sapiens cDNA 5' end similar to neuro-D4 protein
11947	24276	31018	2.92	4.5E-02	11418013	NT	Gallus gallus mRNA for alpha1 integrin, complete cds
12367	24973	30636	6.27	4.5E-02	AA191097.1	EST_HUMAN	Homo sapiens rat finger protein-like 3 (RFPL3), mRNA
237	12897		3.08	4.4E-02	BE9272733.1	EST_HUMAN	zq43f1.1.r1 Stralagene HNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632493 5'
2144	14722		6.8	4.4E-02	P31568	SWISSPROT	801652154F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935388 5'
2532	15096	27688	2.62	4.4E-02	AW875475.1	EST_HUMAN	HYPOTHETICAL PROTEIN (ORF 2280)
3702	16303	28771	1.5	4.4E-02	AF159160.1	NT	QV2-PT0012-010300-070-g02 PT0012 Homo sapiens cDNA
4733	17314	29756	1.23	4.4E-02	AF109907.1	NT	Myxococcus xanthus serine/threonine kinase Pkn10 (pkn10) gene, complete cds
4733	17314	29757	1.23	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
7172	19704	32561	1.56	4.4E-02	AF095824.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
7172	19704	32562	1.56	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
8687	21226	34146	2.04	4.4E-02	AA736969.1	EST_HUMAN	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
10951	23466	36489	4.58	4.4E-02	AF060669.1	NT	mw13h03.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1239221 3'
11080	23592	36629	2.63	4.4E-02	AA496739.1	EST_HUMAN	Hepatitis E virus strain HEV-US2 polypeptide (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds
							ae33704.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897631 5'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11684	24088		3.28	4.4E-02	AB040926.1	NT	Homo sapiens mRNA for KIAA1493 protein, partial cds
813	13431	25936	8.91	4.3E-02	AF003249.1	NT	Microne saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
2803	15185	27732	1.18	4.3E-02	AV704878.1	EST_HUMAN	AV704878 ADB Homo sapiens cDNA clone ADBA0H08 5'
3477	16083	28557	8.12	4.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3720	16321		1.12	4.3E-02	AF060588.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
6822	19219	32023	5.71	4.3E-02	P30427	SWISSPROT	PLECTIN
6822	19219	32024	5.71	4.3E-02	P30427	SWISSPROT	PLECTIN
6830	19420	32236	0.68	4.3E-02	AA852266.1	EST_HUMAN	ns60c12.s1 NCL_CGAP_P2 Homo sapiens cDNA clone IMAGE:1188888
8450	20990	33908	0.74	4.3E-02	AF293359.1	NT	Homo sapiens desmocollin 3 (DSC3) gene, complete cds, alternatively spliced
8738	21275	34186	0.98	4.3E-02	X55322.1	NT	H. sapiens NCAM mRNA for neural cell adhesion molecule
8738	21275	34197	0.98	4.3E-02	X55322.1	NT	H. sapiens NCAM mRNA for neural cell adhesion molecule
899	13471	25982	1.57	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
899	13513		2.24	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
929	13542	26060	0.69	4.2E-02	AW003645.1	EST_HUMAN	wx34g01.x1 NCL_CGAP_P1H Homo sapiens cDNA clone IMAGE:2545584 3' similar to TR:Q63291 Q63291
1758	14348		1.32	4.2E-02	AL445066.1	NT	L1 RETROPOSON, ORF2 MRNA, contains L1.13 L1 L1 repetitive element; Thermoplasma acidophilum complete genome; segment 4/5
3180	15802	28274	0.98	4.2E-02	AI493472.1	EST_HUMAN	q98f10.x1 NCL_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2019787 3' similar to gb:M35718
3728	16327	28794	1.38	4.2E-02	P23081	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR BFR-2 PRECURSOR (HUMAN); TRANSFORMING PROTEIN MAF
4410	16995	29437	1.03	4.2E-02	U26674.1	NT	Saccharomyces cerevisiae general sporulation (GSG1) gene, complete cds
4410	16995	29438	1.03	4.2E-02	U26674.1	NT	Saccharomyces cerevisiae general sporulation (GSG1) gene, complete cds
4854	17432	29883	0.69	4.2E-02	BF342895.1	EST_HUMAN	802017105F1 NCL_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4152672 5'
5802	18427	31145	1.49	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5802	18427	31146	1.49	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7534	20054	32827	5.29	4.2E-02	AF276752.1	NT	Legionella pneumophila catalase-peroxidase (katA) gene, complete cds
8745	21284	34206	3.5	4.2E-02	P05095	SWISSPROT	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
10069	22664	35559	1.17	4.2E-02	Q16650	SWISSPROT	T-BRAIN-1 PROTEIN (T-BRAIN-1) (TBR-1) (TES-56)
10919	23438	38459	3.12	4.2E-02	AA976118.1	EST_HUMAN	on33b11.s1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1559461 3' similar to gb:MB5290
11187	23682	38739	2.3	4.2E-02	BE815822.1	EST_HUMAN	INTERLEUKIN-12 BETA CHAIN PRECURSOR (HUMAN); PM3-BN0174-250500-008-p10 BN0174 Homo sapiens cDNA

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1187	23692	36740	2.3	4.2E-02	BE15822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
11379	23831	36894	2.06	4.2E-02	AF176458.1	NT	PRRS isolate PRRSV36 envelope glycoprotein gene, complete cds
12226	25023		3.4	4.2E-02	AI983494.1	EST_HUMAN	wf49g10.x1 NCI_CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2510850 3'
536	13167	25648	0.7	4.1E-02	AF200629.1	NT	Homo sapiens HPS1 gene, intron 5
2701	15258	27826	2.87	4.1E-02	AE002330.2	NT	Chlamydia muridarum, section 60 of 85 of the complete genome
4571	17154		8.95	4.1E-02	AW893484.1	EST_HUMAN	QV1-NN0012-180400-184-406 NN0012 Homo sapiens cDNA
5295	17857		0.69	4.1E-02	X85880.1	NT	L.monocytogenes type 3 partial lap gene (strain 443)
5824	18448	31170	0.98	4.1E-02	BE251894.1	EST_HUMAN	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
5824	18448	31171	0.98	4.1E-02	BE251894.1	EST_HUMAN	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
6962	19539		0.97	4.1E-02	X75881.1	NT	A.thaliana mRNA for plasma membrane intrinsic protein 1a
7166	19698	32532	1.92	4.1E-02	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
7522	20042	32911	1.76	4.1E-02	7662347	NT	Homo sapiens KIAA0867 protein (KIAA0867), mRNA
							Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit?
7742	20250	33143	3.14	4.1E-02	AF026198.1	NT	CUTICLE COLLAGEN 34
8577	21116	34038	0.56	4.1E-02	P34887	SWISSPROT	EST84291 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
9081	21617	34552	0.85	4.1E-02	AA372398.1	EST_HUMAN	Brassica napus gln gene for plastid glutamine synthetase, exons 1-12
12572	25024	30618	24.9	4.1E-02	AJ271909.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
3281	15892	28371	3.71	4.0E-02	AB040904.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
3868	16466	28929	0.98	4.0E-02	L11910.1	NT	Homo sapiens PTS gene for 8-pyruvoyltetrahydropterin synthase, complete cds
5296	17858	30284	0.58	4.0E-02	AB042297.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5581	18212	30661	5.51	4.0E-02	AF280107.1	NT	7n52h07.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3568380 3' similar to TR:O75296 O75296
6362	18966	31744	1.66	4.0E-02	BF110434.1	EST_HUMAN	R29124_1.1
							Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
7678	20189	33078	5.8	4.0E-02	L23838.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7743	20251	33144	0.87	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7743	20251	33145	0.87	4.0E-02	AB000381.1	NT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
8651	21190	34108	2.64	4.0E-02	P08640	SWISSPROT	
9562	22062		0.84	4.0E-02	BF679376.1	EST_HUMAN	602153884F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294724 5'
9566	22066	35051	3.35	4.0E-02	AJ000941.1	NT	Methanobacterium thermoautotrophicum strain Marburg, Thiol:fumarate reductase subunit A

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9895	22392		1.28	4.0E-02	D43949.1	NT	Human mRNA for KIAA0082 gene, partial cds
11608	24031		1.62	4.0E-02	AJ001018.1	NT	Khuyveromyces lactis gene for Car+ ATPase
11841	24834	30796	18.69	4.0E-02	AJ001056.1	NT	Ovis aries mRNA for acetyl-CoA carboxylase
1159	13762	26273	3.8	3.9E-02	BF516149.1	EST_HUMAN	UI-HBW1-ant-h-08-0-UI.s1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
1390	13984	26510	1.88	3.9E-02	P41047	SWISSPROT	FAS ANTIGEN LIGAND
2004	14598	27145	2.67	3.9E-02	AJ403386.1	NT	Mimusculus DNA for desmin-binding fragment DesD7
2728	15283		1.85	3.9E-02		NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
5325	17887	30303	0.8	3.9E-02	AW382417.1	EST_HUMAN	RC6-ST0258-171199-021-C09 ST0258 Homo sapiens cDNA
5344	17805	30320	1.14	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5344	17805	30321	1.14	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5687	18313	30810	0.73	3.9E-02	D50608.1	NT	Rat gene for cholecystokinin type-A receptor (CCKAR), complete cds
5687	18313	30811	0.73	3.9E-02	D50608.1	NT	Rat gene for cholecystokinin type-A receptor (CCKAR), complete cds
5906	18528	31254	1.24	3.9E-02	BE66841.1	EST_HUMAN	601649874F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933642 5'
6018	18637	31377	0.68	3.9E-02	BE675203.1	EST_HUMAN	602138132F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274910 5'
7118	19458	32273	1.01	3.9E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
7781	20324	33229	0.93	3.9E-02	BF239613.1	EST_HUMAN	60180648F1 NIH_MGC_64 Homo sapiens cDNA clone IMAGE:4134778 5'
8004	20546	33449	0.56	3.9E-02	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
8004	20546	33450	0.56	3.9E-02	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
11287	20286	33188	1.6	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
11691	24981		7.19	3.9E-02	AB042553.1	NT	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds
12373	24543		1.73	3.9E-02	U66061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV18S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2.>
12503	24902		64.84	3.9E-02	AL049868.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxq28orf
1985	14577	27137	1.24	3.8E-02	BE885137.1	EST_HUMAN	601510891F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912215 5'
4997	17571	30015	0.99	3.8E-02	BE383275.1	EST_HUMAN	601308488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3626757 5'
4997	17571	30016	0.99	3.8E-02	BE383275.1	EST_HUMAN	601308488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3626757 5'
5062	17635	30078	0.93	3.8E-02	AU124122.1	EST_HUMAN	AU124122 NT2RM2 Homo sapiens cDNA clone NT2RM2001698 5'
5832	18281	30733	1.19	3.8E-02	M11228.1	NT	Human protein C gene, complete cds
6237	18846	31617	1.07	3.8E-02	P10284	SWISSPROT	HOMEBOX PROTEIN HOX-B4 (HOX-2.6)
7359	19885	32748	1.43	3.8E-02	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8598	21137		1.3	3.8E-02	M6075.1	NT	Human von Willebrand factor gene, exons 23 through 34
10506	23000		0.47	3.8E-02	AE001329.1	NT	Chlamydia trachomatis section 56 of 87 of the complete genome
10532	23069	36082	2.17	3.8E-02	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
1029	13639	26154	3.69	3.7E-02	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
1432	14025	26553	1.15	3.7E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
2278	14852	27430	4.49	3.7E-02	AI984806.1	EST_HUMAN	w85e08.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494502 3'
2613	15175	27743	0.93	3.7E-02	AB018261.1	NT	Homo sapiens mRNA for KIAA0718 protein, partial cds
3088	15701	28174	0.97	3.7E-02	P79944	SWISSPROT	EOMESODERMIN
3088	15703	28175	4.74	3.7E-02	BF312963.1	EST_HUMAN	601896233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125584 5'
7138	25118		0.73	3.7E-02	AP000063.1	NT	Aeropyrum pernix genomic DNA, section 67
9928	22424		0.89	3.7E-02	AA782516.1	EST_HUMAN	ai55c09.s1 Soares parathyroid_tumor_NbHPA Homo sapiens cDNA clone 1360812 3'
11735	24139	37156	7.99	3.7E-02	BF124974.1	EST_HUMAN	601782117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973 5'
12435	24668	30707	3.02	3.7E-02	11418392	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
3715	16316	28784	0.82	3.6E-02	X73221.1	NT	H. vulgare Sst1 gene for sucrose synthase
3723	16324	28791	0.87	3.6E-02	AL096806.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10(10q26.3) of Homo sapiens
5620	18249	30701	0.77	3.6E-02	X59403.1	NT	C-glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5620	18249	30717	0.77	3.6E-02	X59403.1	NT	C-glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
6808	19399	32213	5.32	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
6808	19399	32214	5.32	3.6E-02	AW945516.1	EST_HUMAN	CM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
7143	19678	32516	1.68	3.6E-02	AF025952.1	NT	Chromatium vinosum sulfur globule protein Cyt2 precursor (sgp2) gene, complete cds
7347	19873	32739	3.52	3.6E-02	AA714521.1	EST_HUMAN	rw20e05.s1 NCL CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb:J00314_rna2
7629	20141	33020	0.96	3.6E-02	BE143078.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
9313	21827	34776	1.87	3.6E-02	U20608.1	NT	MRO-HT0158-030200-003-b08 HT0158 Homo sapiens cDNA
9313	21827	34777	1.87	3.6E-02	U20608.1	NT	Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9530	22030	34989	0.72	3.6E-02	BF347586.1	EST_HUMAN	Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
928	13541	26059	1.57	3.5E-02	U09506.1	NT	602020453F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156116 5'
1046	13654	26166	2.29	3.5E-02	AF253417.1	NT	Drosophila melanogaster liggrin mRNA, complete cds
						NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds

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Probe SEQ ID NO.	Exon ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1610	14203	26736	1.49	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248377 5'
1610	14203	26737	1.49	3.5E-02	BF678085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248377 5'
4293	16879	29326	1.91	3.5E-02	AE001773.1	NT	Thermotoga maritima section 85 of 136 of the complete genome
4406	16991	29435	1.16	3.5E-02	P53780	SWISSPROT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
6370	16974	31752	2.11	3.5E-02	J01238.1	NT	Maize actin 1 gene (MAc1), complete cds
7918	20460		0.82	3.5E-02	H29951.1	EST_HUMAN	yp44a05.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:190256 5' similar to contains Alu repetitive element;
8558	21097	34018	3.5	3.5E-02	BE959970.1	EST_HUMAN	801644701R2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3928737 3'
9631	22427	35401	2.44	3.5E-02	X76642.1	NT	Llactis MG1363 grpE and dnaK genes
9977	22472	35455	0.49	3.5E-02	BE561042.1	EST_HUMAN	601344661F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677654 5'
11367	23819	36880	1.92	3.5E-02	AW861641.1	EST_HUMAN	PM1-CT0328-291299-002-h03 CT0328 Homo sapiens cDNA
11367	23819	36881	1.92	3.5E-02	AW861641.1	EST_HUMAN	PM1-CT0328-291299-002-h03 CT0328 Homo sapiens cDNA
12357	24534		1.39	3.5E-02	AF009683.1	NT	Homo sapiens T cell receptor beta locus, TCRBV85P to TCRBV21S2A2 region
12429	24913		4.38	3.5E-02	BE276948.1	EST_HUMAN	601178785F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543833 5'
604	13233	25706	1.18	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
604	13233	25707	1.18	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
605	13233	25706	3.27	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
605	13233	25707	3.27	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1098	13684	26203	3.22	3.4E-02	AW274020.1	EST_HUMAN	xy28d07.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814253 3' similar to
1248	13845		6.54	3.4E-02	11345459	NT	SW: C211_HUMAN P53801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR ;
							Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
2435	15002	27574	1.82	3.4E-02	T57160.1	EST_HUMAN	yc20e08.r1 Stratagene lung (H937210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains
3478	16084	28559	1.11	3.4E-02	AL163208.2	NT	MER28 repetitive element
3843	16442	28903	0.88	3.4E-02	BE839514.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C008
3893	16591	29063	4.29	3.4E-02	AW1794952.1	EST_HUMAN	RC3-FN0155-060700-011-d10 FN0155 Homo sapiens cDNA
4703	17285	29730	3.17	3.4E-02	X59796.1	NT	RC6-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA
5217	17782		2.61	3.4E-02	Q26457	SWISSPROT	M.musculus S-antigen gene promoter region
5237	17801	30220	1.47	3.4E-02	AJ012469.1	NT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
6353	18958		0.88	3.4E-02	BF131628.1	EST_HUMAN	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6638	18046	30498	4.63	3.4E-02	U24393.1	NT	601820445F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052434 5'
8204	20745		3.76	3.4E-02	AJB69829.1	EST_HUMAN	Homo lysyl oxidase-like protein gene, exon 3
							wb99d04.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2433031 3'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8882	21221	34141	1.64	3.4E-02	AA684886.1	EST_HUMAN	nu70708.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1216071 similar to contains Alu repetitive element; contains element MER25 MER25 repetitive element:
8848	21387		5.71	3.4E-02	AA194308.1	EST_HUMAN	zq04f11.s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:628749 3' similar to TR:G1017425 G1017425
9883	22192		0.53	3.4E-02	A1092719.1	EST_HUMAN	IPISGKPLPKVTLSDRGVPLKATMRPNTITAENLTINKESVTADAGRYEITTAANSSGTTKAFINIVLDRPG PPT GPVIVSDITEESVTLKWEPPKYDGGQVNTYLLKRETSTAVVTEVSA TVARTMMKVAKL ...;
395	13041		11.74	3.3E-02	AA398735.1	EST_HUMAN	oz98h08.x1 Soares_paritydrol_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1683519 3'
1209	13809	26322	18.12	3.3E-02	AB035887.1	NT	z75608.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728198 3'
1681	14273	28808	1.29	3.3E-02	AF110783.1	NT	Cricetulus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds
1775	14365		1.28	3.3E-02	AE000700.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
2131	14709		2.05	3.3E-02	R09112.1	EST_HUMAN	Aquifex aeolicus section 32 of 109 of the complete genome
3408	18015	28494	0.85	3.3E-02	H02389.1	EST_HUMAN	y25c09.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:127888 5'
4256	14273	28808	2.91	3.3E-02	AF110783.1	NT	y35h02.r1 Soares_placenta_Nb2HP Homo sapiens cDNA clone IMAGE:150771 5'
4566	17149	29596	2.15	3.3E-02	BF245995.1	EST_HUMAN	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
6591	19159	31956	26.84	3.3E-02	BF245995.1	EST_HUMAN	Mus musculus tumor rejection antigen gp96 (Tra1), mRNA
6561	19159	31957	26.84	3.3E-02	BF245995.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
9246	21772	34721	0.73	3.3E-02	BF115621.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
9246	21772	34722	0.73	3.3E-02	BF115621.1	EST_HUMAN	7m92d04.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3562423 3'
9345	21859	34807	0.59	3.3E-02	AA488202.1	EST_HUMAN	7m92d04.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3562423 3'
9345	21859	34808	0.59	3.3E-02	AA488202.1	EST_HUMAN	ad08f09.s1 Soares_NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1 MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
10491	22985		0.5	3.3E-02	H38109.1	EST_HUMAN	ad08f09.s1 Soares_NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1 MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
11000	23514	36548	3.5	3.3E-02	BF091107.1	EST_HUMAN	y651f11.s1 Soares_retina_N2b4HR Homo sapiens cDNA clone IMAGE:190989 3'
11932	24266		2.14	3.3E-02	T96545.1	EST_HUMAN	602247171F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332497 5'
12089	24358		2.05	3.3E-02	M81890.1	NT	y649f11.r1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:121101 5'
137	12802	25291	1.87	3.2E-02	AJ002005.1	NT	Human interleukin 11 (IL11) gene, complete mRNA
1165	13767	26277	19.04	3.2E-02	AF096275.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
1165	13767	26278	19.04	3.2E-02	AF096275.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
1808	14398	28943	1.36	3.2E-02	AF128894.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
2164	14741		1.35	3.2E-02	P28955	SWISSPROT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
2865	12802	25291	0.59	3.2E-02	AJ002005.1	NT	LARGE TEGUMENT PROTEIN
3168	15782	28253	12.01	3.2E-02	BE667353.1	EST_HUMAN	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
							601442431F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846727 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3776	16376	28842	1.3	3.2E-02	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4298	16885		20.05	3.2E-02	X94768.1	NT	H.sapiens RP3 gene (XLRP gene 3)
4882	17457	29809	3.35	3.2E-02	AF114182.1	NT	Saxifraga nidifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
5726	18352	31055	1.45	3.2E-02	X68708.1	NT	S.griseocarneum whiG-Stv gene
5726	18352	31056	1.45	3.2E-02	X68708.1	NT	S.griseocarneum whiG-Stv gene
6846	18242	32045	2.59	3.2E-02	M32437.1	NT	Rat/polyomavirus left junction in cell line W98.14
6847	18243		27.51	3.2E-02	T89387.1	EST_HUMAN	y433h12.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains
6722	19316	32119	3.78	3.2E-02	AF173845.1	NT	Alu repetitive element contains LTR1 repetitive element
7739	20247	33140	0.85	3.2E-02	11424049	NT	Saginus oedipus tissue kallikrein gene, complete cds
8242	20783	33702	13.08	3.2E-02	8680565	NT	Homo sapiens cytochrome P450, subfamily 11B (phenobarbital-inducible) (CYP2B), mRNA
8871	21410		0.69	3.2E-02	AF109718.1	NT	Mus musculus kinesin family member 3c (Kif3c), mRNA
9152	21687	34630	1.06	3.2E-02	A1278971.1	EST_HUMAN	Homo sapiens chromosome 3 subtelomeric region
9152	21687	34631	1.06	3.2E-02	A1278971.1	EST_HUMAN	qm17b04.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
9969	22484		4.05	3.2E-02	AA719795.1	EST_HUMAN	qm17b04.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
10280	22755	35743	0.95	3.2E-02	U96782.1	NT	z954b12.s1 Soares pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:1882063 3'
1303	13887		1.8	3.1E-02	4503416	NT	gbL08441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN);
1348	13943	26486	1.26	3.1E-02	P18845	SWISSPROT	Mecaca mulatta chemokine receptor CCR5 mRNA, complete cds
1936	14520	27076	1.52	3.1E-02	8671564	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
2017	14599		1.14	3.1E-02	Z50097.1	NT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
5207	17772		0.87	3.1E-02	BE091869.1	EST_HUMAN	Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
5331	17892		3.09	3.1E-02	AL161550.2	NT	Drosophila melanogaster mRNA for headcase protein
5371	16916		0.98	3.1E-02	AU119006.1	EST_HUMAN	IL2-BT0733-130400-067-A08 BT0733 Homo sapiens cDNA
5468	18102	30421	1.13	3.1E-02	U78104.1	NT	Arabidopsis thaliana DNA chromosome 4, centig fragment No. 50
5953	18194		2.32	3.1E-02	AA278478.1	EST_HUMAN	AU119008 HEMBA1 Homo sapiens cDNA clone HEMBA1004842 5'
5826	18433	31176	0.8	3.1E-02	BF687742.1	EST_HUMAN	Human leukemia inhibitory factor receptor (LIFR) gene, promoter and partial exon 1
9944	22439	35417	3.63	3.1E-02	AF034779.1	NT	zs81a08.r1 NCI_CGAP_GCBT Homo sapiens cDNA clone IMAGE:703858 5'
12667	24737		2.24	3.1E-02	AW468414.1	EST_HUMAN	602066783F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4086789 5'
1864	14257		2.3	3.0E-02	AF187125.1	NT	Enterococcus faecalis surface protein precursor, gene, complete cds
2621	15193	27749	0.9	3.0E-02	AA402242.1	EST_HUMAN	hcs3767.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2921221 3'
3623	16226	28704	1.24	3.0E-02	M94176.1	NT	Phyoketines minutus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
						EST_HUMAN	zf65h03.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:727253 5'
						NT	Saccharomyces cerevisiae stem-loop mutation suppressor SSL2 gene, complete cds

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3714	16315	28783	3.07	3.0E-02	AF247644.1	NT	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3808	18407		0.79	3.0E-02	AW820223.1	EST_HUMAN	QV2-ST0296-150200-040-e09 ST0296 Homo sapiens cDNA
4021	16619		0.74	3.0E-02	AA364003.1	EST_HUMAN	EST174530 Pineal gland II Homo sapiens cDNA 5' end
5000	17573	30017	1.04	3.0E-02	BE782830.1	EST_HUMAN	601472331F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3875503 5'
5208	17773	30195	7.49	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5208	17773	30196	7.49	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5303	17865	30289	1.1	3.0E-02	BE968917.1	EST_HUMAN	601849872R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933928 3'
5590	18221		3.62	3.0E-02	AB046793.1	NT	Homo sapiens mRNA for KIAA1573 protein, partial cds
6402	19005	31784	0.76	3.0E-02	N96615.1	EST_HUMAN	za39a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294906 5' similar to contains element TAR1 repetitive element
6402	19005	31785	0.76	3.0E-02	N96615.1	EST_HUMAN	za39a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294906 5' similar to contains element TAR1 repetitive element
6884	19619	32453	2.93	3.0E-02	AJ242906.1	NT	Cyprinus carpio mRNA for inducible nitric oxide synthase (iNOS) gene
6967	19485	32306	3.15	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
6967	19485	32307	3.15	3.0E-02	BE889948.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
7131	19471	32290	1.93	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7131	19471	32291	1.93	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7262	19810	32666	1.32	3.0E-02	M86524.1	NT	Human dystrophin gene
7563	20098		0.76	3.0E-02	BF246361.1	EST_HUMAN	601854861F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4074548 5'
8575	21114	34033	0.79	3.0E-02	BF333889.1	EST_HUMAN	IL5-HT0704-290800-108-c04 HT0704 Homo sapiens cDNA
8728	21267		1.77	3.0E-02	AF275654.1	NT	Omithorhynchus anatinus coagulation factor X mRNA, complete cds
10357	22851	35845	1.46	3.0E-02	AE001797.1	NT	Thermotoga maritima section 109 of 136 of the complete genome
10441	22935	35944	0.46	3.0E-02	Z21211.1	EST_HUMAN	HSAAADTHS TEST1, Human adult Testis tissue Homo sapiens cDNA clone cam test244 (b)
11111	23621	36662	4.11	3.0E-02	M81357.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
11538	23986	37057	8.47	3.0E-02	AA483216.1	EST_HUMAN	ne8704.s1 NCL_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911283
12043	25076	30515	2.56	3.0E-02	R32019.1	EST_HUMAN	yh63d04.s1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:134407 3'
12417	24570		18.42	3.0E-02	AW895665.1	EST_HUMAN	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA
12460	25069		3.53	3.0E-02	AF048687.1	NT	Rattus norvegicus UDP-Gal-glucosyltransferase beta-1,4-galactosyltransferase mRNA, complete cds
2479	15467	27614	1.05	2.9E-02	AF228703.1	NT	Homo sapiens mitochondrial glutathione reductase and cytosolic glutathione reductase (GRD1) gene, complete cds, alternatively spliced
3021	15637	28114	1.11	2.9E-02	BE565644.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3021	15637	28115	1.11	2.9E-02	BE585644.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'
3616	16219	28698	0.84	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
4003	16601	29075	0.69	2.9E-02	H72805.1	EST_HUMAN	y407e10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233130 5'
5272	18016		62.36	2.9E-02	R09112.1	EST_HUMAN	yf25c09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127888 5'
6213	18823	31594	1.31	2.9E-02	AF060221.1	NT	Sus scrofa deoxyribonuclease II mRNA, complete cds
6434	19037	31824	6.5	2.9E-02	BF032233.1	EST_HUMAN	601452861F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:385589 5'
7296	19824	32683	10.37	2.9E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
7455	19879	32845	0.67	2.9E-02	D28214.1	EST_HUMAN	HUMNK262 Human epidermal keratinocyte Homo sapiens cDNA clone 262
7640	20482	33393	0.91	2.9E-02	AF129279.1	NT	Buchnera aphidicola natural-host Schlechtendalia chinensis glucuronate-6-phosphate dehydrogenase (gnd) gene, partial cds
7640	20482	33394	0.91	2.9E-02	AF129279.1	NT	Buchnera aphidicola natural-host Schlechtendalia chinensis glucuronate-6-phosphate dehydrogenase (gnd) gene, partial cds
9577	22077	35040	2.16	2.9E-02	AW875979.1	EST_HUMAN	CM3-PT0014-071289-051-c04 PT0014 Homo sapiens cDNA
9577	22077	35041	2.16	2.9E-02	AW875978.1	EST_HUMAN	CM3-PT0014-071289-051-c04 PT0014 Homo sapiens cDNA
9788	22286		0.59	2.9E-02	AW976597.1	EST_HUMAN	EST388706 IMAGE resequences, MAGN Homo sapiens cDNA
10247	22742	35732	0.94	2.9E-02	AP000084.1	NT	Aeropyrum pernix genomic DNA, section 7/7
10925	16219	28698	1.73	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
12045	24979		1.88	2.9E-02	AU135817.1	EST_HUMAN	AUT35817 PLACE1 Homo sapiens cDNA clone PLACE1002982 5'
591	13221		0.99	2.8E-02	AW970153.1	EST_HUMAN	EST382234 IMAGE resequences, MAGN Homo sapiens cDNA
3414	16022	28502	1.62	2.8E-02	AF068063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
3414	16022	28503	1.62	2.8E-02	AF068063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
4401	16886		0.71	2.8E-02	6393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
5337	17898	30313	0.92	2.8E-02	N87073.1	EST_HUMAN	L2083F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone L2083 5' similar to TRNA-
5979	18306	30802	11.28	2.8E-02	BE741083.1	EST_HUMAN	GUANINE TRANSGLYCOSYLASE
6900	19634	32472	1.14	2.8E-02	T76960.1	EST_HUMAN	601594078F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948067 5'
8270	20811	33732	1.6	2.8E-02	AJ005820.1	NT	y421b08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108855 5'
8947	21485	34407	0.74	2.8E-02	AA280762.1	EST_HUMAN	Gratostigma plantagineum mRNA for homeodomain leucine zipper protein (hb-1)
9135	21670	34612	0.91	2.8E-02	AF187872.1	NT	zs96c06.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711466 5'
9237	21763	34709	0.64	2.8E-02	AE001092.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, complete cds
10498	22962	36002	1.81	2.8E-02	BF527244.1	EST_HUMAN	Archaeoglobus fulgidus section 15 of 172 of the complete genome
3478	16085	28559	4.18	2.7E-02	AL161494.2	NT	602039477F2 NCI CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4177267 5'
4280	16868	29312	1.91	2.7E-02	N47258.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
4280	16866	29313	1.91	2.7E-02	N47258.1	EST_HUMAN	y66h12.r1 Soares, multiple sclerosis_2NBMSP Homo sapiens cDNA clone IMAGE:280487 5'
4280	16866	29313	1.91	2.7E-02	N47258.1	EST_HUMAN	y66h12.r1 Soares, multiple sclerosis_2NBMSP Homo sapiens cDNA clone IMAGE:280487 5'

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5633	18282	30734	1.11	2.7E-02	R12245.1	EST_HUMAN	yf33d09.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:128657 5' similar to
6061	18678	31420	0.7	2.7E-02	X61670.1	NT	SP:JC2264.JC2264 TISSUE FACTOR PATHWAY INHIBITOR - RHESUS ;
6713	19307		0.9	2.7E-02	X97580.1	NT	T.aestivum pTTH20 mRNA for wheat type V thionin
7127	19487	32285	2.06	2.7E-02	AA93571.1	EST_HUMAN	A.bisporus pika gene
8285	20836		1.21	2.7E-02	AI377036.1	EST_HUMAN	ot96103.s1 Soares fetal Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1624661 3'
597	13226	25700	1.52	2.6E-02	AL163282.2	NT	tc28g08.x1 Soares total fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2085982 3' similar to
2404	14972	27544	2.79	2.6E-02	AA490021.1	EST_HUMAN	contains Alu repetitive element
2406	14974	27546	7.33	2.6E-02	6754241	NT	Homo sapiens chromosome 21 segment HS21C082
2406	14974	27547	7.33	2.6E-02	6754241	NT	ab02b02.s1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839595 3'
2940	15556		1.17	2.6E-02	AF109006.1	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
5031	17605	30049	4.74	2.6E-02	L12032.1	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
5224	17798	30208	1.58	2.6E-02	AE002014.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf, C2, G9A, NG22, G9, HSP70, HSP70, HSC70, and smRNP genes, complete cds; G7A gene, partial cds; and unknown genes
5254	17817	30241	2.34	2.6E-02	AW241154.1	EST_HUMAN	Chicken dorsalis-1 mRNA, complete cds
6368	18972		6.32	2.6E-02	AI206030.1	EST_HUMAN	Deinococcus radiodurans R1 section 151 of 229 of the complete chromosome 1
6556	19154	31850	2.29	2.6E-02	BE621748.1	EST_HUMAN	xa52b04.x1 NCI_CGAP_Sar4 Homo sapiens cDNA clone IMAGE:2570383 3' similar to SW.Y069_HUMAN
6915	19574	32402	0.75	2.6E-02	Z99084.1	NT	Q15041 HYPOTHETICAL PROTEIN KIAA0089 ;
6915	19574	32403	0.75	2.6E-02	Z99084.1	NT	qg27f11.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1762317 3'
6980	19488	32310	6.45	2.6E-02	8981271	NT	601493473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3'
8442	20982	33887	0.77	2.6E-02	AA860946.1	EST_HUMAN	Vaccinia virus ORF1L, strain W yeth
9282	21882	34827	1.41	2.6E-02	11432020	NT	Vaccinia virus ORF1L, strain W yeth
9630	22130	35094	0.6	2.6E-02	AF114952.1	NT	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA
9630	22130	35095	0.6	2.6E-02	AF114952.1	NT	ak22f04.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1406719 3'
10302	22796	35787	4.1	2.6E-02	AL163303.2	NT	Homo sapiens KIAA1070 protein (KIAA1070), mRNA
11265	23793		2.44	2.6E-02	AA279351.1	EST_HUMAN	Saccharomyces dairenensis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene
11437	23887	36955	1.63	2.6E-02	AW500547.1	EST_HUMAN	Saccharomyces dairenensis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene
11965	25060	30512	1.26	2.6E-02	BF343827.1	EST_HUMAN	encoding mitochondrial protein, complete cds
12083	24354		1.29	2.6E-02	11422836	NT	Homo sapiens chromosome 21 segment HS21C103
557	13188	25666	1.76	2.5E-02	AI793130.1	EST_HUMAN	z884d02.1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704162 5'
							UI-HF-BNO-akj-10-0-UJr1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077469 5'
							602015501F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4150944 5'
							Homo sapiens hypothetical protein FLJ10724 (FLJ10724), mRNA
							on28f06.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
567	13188	25667	1.76	2.5E-02	A1793130.1	EST_HUMAN	on26f06.y6 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
842	13458	25987	19.68	2.5E-02	BE974314.1	EST_HUMAN	601880305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'
902	13518	26034	4.48	2.5E-02	BE974314.1	EST_HUMAN	601880305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950665 3'
2791	15344		2.84	2.5E-02	U12571.1	NT	Rattus norvegicus rabphilin-3A mRNA, complete cds
2983	15599	28076	3.52	2.5E-02	X99697.1	NT	H. carterae mRNA for fucosanthin chlorophyll a/c binding protein, Fcp1
2983	15599	28079	3.52	2.5E-02	X99697.1	NT	H. carterae mRNA for fucosanthin chlorophyll a/c binding protein, Fcp1
4119	18005	29187	0.77	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4119	18005	29169	0.77	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4284	18870	29316	5.25	2.5E-02	AW592114.1	EST_HUMAN	h93h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2934015 3'
5989	18512	31238	0.7	2.5E-02	A1732776.1	EST_HUMAN	z83c10.x5 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:810354 3'
6340	18946		4.9	2.5E-02	BE670128.1	EST_HUMAN	7a30a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L.11 L1 repetitive element
6357	18961		4.3	2.5E-02	BE746888.1	EST_HUMAN	601579393F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928054 5'
6478	19079	31862	0.72	2.5E-02	L29029.1	NT	Chlamydomonas reinhardtii VSP-3 mRNA, complete cds
7660	20172	33058	1.52	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4213406 5'
7660	20172	33059	1.52	2.5E-02	BF526722.1	EST_HUMAN	602070562F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4213406 5'
7820	20462	33368	0.48	2.5E-02	BE252469.1	EST_HUMAN	601108291F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3344278 5'
8759	21298	34219	0.93	2.5E-02	Q91713	SWISSPROT	GHORDIN PRECURSOR (ORGANIZER-SPECIFIC SECRETED DORSALIZING FACTOR)
8894	21432	34355	0.45	2.5E-02	AW025821.1	EST_HUMAN	wu08c10.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:2516370 3'
9978	22473		0.8	2.5E-02	X71303.1	NT	D radicum 28S ribosomal RNA, D2 domain
10475	22869	35978	0.73	2.5E-02	A147615.1	EST_HUMAN	q52a208.x1 Soares_pregnant uterus NBHPU Homo sapiens cDNA clone IMAGE:1696982 3'
10889	23219	36231	2.04	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME I
10889	23219	36232	2.04	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME I
							Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II beta chain (IEbeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-like
10761	23285		4.04	2.5E-02	AF050157.1	NT	Homo sapiens gene for LECT2, complete cds
11602	24045		1.73	2.5E-02	AB007546.1	NT	Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC63634), mRNA
11922	24993		3.33	2.5E-02	11420078	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
12115	24855		1.53	2.5E-02	11433220	NT	Homo sapiens discoidin domain putative protein kinase Mica (mika) gene, complete cds
12215	24438		2.17	2.5E-02	U60169.1	NT	Dicotyledon discoidin domain putative protein kinase Mica (mika) gene, complete cds
12242	24454	30957	1.31	2.5E-02	BE973327.1	EST_HUMAN	601652365R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935513 3'
185	12846	25332	0.75	2.4E-02	A1378592.1	EST_HUMAN	tc72c07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2070158 3'
1842	14234	28768	2.09	2.4E-02	H65884.1	EST_HUMAN	y75f11.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:211149 5'
2088	15457	27239	2.02	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2088	15457	27240	2.02	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4458	17044	29487	1.89	2.4E-02	J06110.1	NT	T. thermophila calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds
4619	17202	29650	1.83	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4619	17202	29651	1.83	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
6363	18987	31745	0.94	2.4E-02	W86680.1	EST_HUMAN	zh63h04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416791 3'
7273	19801	32658	1.06	2.4E-02	Z20573.1	EST_HUMAN	HSAAACKVX T, Human adult Rhabdomyosarcoma cell-line Homo sapiens cDNA
7287	19815	32672	0.95	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
7287	19815	32673	0.95	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
7831	20373		0.69	2.4E-02	AW813007.1	EST_HUMAN	RC3-ST0198-230300-019-h06 ST0196 Homo sapiens cDNA
7884	20426		0.6	2.4E-02	M16780.1	NT	Human retrotransposon 3' long terminal repeat
8379	20919		0.86	2.4E-02	H78376.1	EST_HUMAN	yt12c05.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233576 3' similar to contains Alu repetitive element; contains A3R repetitive element ;
8468	21008	33925	10.74	2.4E-02	N69442.1	EST_HUMAN	za35g11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294596 3' similar to gb K02909 RATSR7K Rat (RNA); contains A3R.b1 A3R repetitive element ;
8917	21455	34375	0.54	2.4E-02	AE001125.1	NT	Borrelia burgdorferi (section 11 of 70) of the complete genome
8939	21477	34398	0.75	2.4E-02	AA625680.1	EST_HUMAN	zu91c06.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745354 3' similar to gb J04422 SLET AMYLOID POLYPEPTIDE PRECURSOR (HUMAN); contains Alu repetitive element; contains element XTR
9720	22218	35193	2.76	2.4E-02	AV692854.1	EST_HUMAN	XTR repetitive element ;
9801	22388	35366	2.9	2.4E-02	AA493894.1	EST_HUMAN	AV692854 GK Homo sapiens cDNA clone GKQDS003 5'
							rh07b12.s1 NCJ CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943583 similar to contains Alu repetitive element; contains element P TR5 repetitive element ;
11447	23897	36962	1.9	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70i gene, partial cds; smRNP, G7A, NG23, MuS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
11447	23897	36963	1.9	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70i gene, partial cds; smRNP, G7A, NG23, MuS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
11718	24127		3.56	2.4E-02	9627909	NT	Bacteriophage b167, complete genome
11898	24222	31044	2.48	2.4E-02	6753635	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
11924	24259	31013	1.36	2.4E-02	BE928869.1	EST_HUMAN	MRO-FT0175-310800-202-a06 FT0175 Homo sapiens cDNA
11984	24294	30981	1.38	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor I (cAMP-GEFI) mRNA, complete cds
11984	24294	31025	1.38	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor I (cAMP-GEFI) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12184	24404		8.87	2.4E-02	AB008569.1	NT	Caenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds
12191	24422		2.11	2.4E-02	N42880.1	EST_HUMAN	Y08A06.1 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:270610 5'
12187	24425		1.55	2.4E-02	BF079477.1	EST_HUMAN	602153281F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4284173 5'
12362	24827	30795	1.48	2.4E-02	AA179693.1	EST_HUMAN	zp13h01.1 Strategic fetal retina 937202 Homo sapiens cDNA clone IMAGE:609361 5'
1913	14488		5.46	2.3E-02	W05340.1	EST_HUMAN	za84g08.1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:289294 5'
1931	14515		21.68	2.3E-02	U94195.1	NT	4 Homo sapiens mammary tumor-associated protein INT8 (INT8) gene, exon 4
2053	14634	27205	0.88	2.3E-02	AW797355.1	EST_HUMAN	CM2-UM0038-290400-172-b11 UM0038 Homo sapiens cDNA
2369	14657	27529	2.31	2.3E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
3745	16346	28814	6.21	2.3E-02	Z20377.1	EST_HUMAN	HSAACADH P. Human foetal Brain Whole tissue Homo sapiens cDNA
3777	16377		0.82	2.3E-02	L23428.1	NT	Canis beta-galactosidase-binding lectin (LGALS3) mRNA, 3' end
4230	16818	28266	0.75	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4230	16818	28267	0.75	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4511	17065	28542	1.21	2.3E-02	AW899107.1	EST_HUMAN	CM4-NN0080-280400-160-b04 NN0080 Homo sapiens cDNA
4548	17130	28574	0.91	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010600-318-g07 MT0118 Homo sapiens cDNA
4548	17130	28575	0.91	2.3E-02	BE935225.1	EST_HUMAN	CM3-MT0118-010600-318-g07 MT0118 Homo sapiens cDNA
4547	18008	29576	1.05	2.3E-02	AW593693.1	EST_HUMAN	xs25d08.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770871 3'
4547	18008	29577	1.05	2.3E-02	AW593693.1	EST_HUMAN	xs25d08.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770871 3'
4688	17280	29726	2.96	2.3E-02	BF026487.1	EST_HUMAN	601872279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
4698	17280	29727	2.96	2.3E-02	BF026487.1	EST_HUMAN	601872279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
5182	17748	30177	0.93	2.3E-02	AW844307.1	EST_HUMAN	RC2-CN0051-290100-011-a07 CN0051 Homo sapiens cDNA
5368	17928	30342	2.72	2.3E-02	A1038076.1	EST_HUMAN	cc21c10.x1 Soares_fetal_liver_spleen_INFILS_S1 Homo sapiens cDNA clone IMAGE:1656978 3' similar to gb:X69908.1 rat1 ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (HUMAN);
5578	18208	30859	3.34	2.3E-02	U86303.1	NT	Caulobacter crescentus topoisomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA carboxylase beta chain (pcdB) homolog gene, partial cds
6733	19327	32132	4.43	2.3E-02	AL161505.2	NT	A. nidulans thaliana DNA chromosome 4, contig fragment No. 17
7056	18075	30428	0.88	2.3E-02	BE141475.1	EST_HUMAN	MIR0-4170080-011069-002-c08 HT0080 Homo sapiens cDNA
7817	20360	33266	6	2.3E-02	U63610.1	NT	Human plectin (PLEC1) gene, exons 3-32, and complete cds
8407	20947	33867	0.74	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8407	20947	33868	0.74	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8630	21169	34085	0.83	2.3E-02	A1695390.1	EST_HUMAN	wa76h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
8630	21169	34086	0.83	2.3E-02	A1695390.1	EST_HUMAN	wa76h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
9065	21802	34532	0.81	2.3E-02	P41068	SWISSPROT	HYPOPHOSPHATASE 55.6 KD PROTEIN B0280.5 IN CHROMOSOME III PRECURSOR
9773	22271	35256	0.72	2.3E-02	P50532	SWISSPROT	CHROMOSOME ASSEMBLY PROTEIN XCAP-C

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9843	22438	35415	1.4	2.3E-02	AE000189.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
9843	22438	35416	1.4	2.3E-02	AE000189.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
10861	23193	36208	2.37	2.3E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
11628	24070		1.67	2.3E-02	AF159132.1	NT	Metapneumovirus ensis fushi tarazu-factor 1 mRNA, complete cds
11846	24843		5.2	2.3E-02	BE278331.1	EST_HUMAN	601178958F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3546567 5'
12282	24485	30940	1.59	2.3E-02	BF528462.1	EST_HUMAN	602043629F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181454 5'
12282	24485	30941	1.59	2.3E-02	BF528462.1	EST_HUMAN	602043629F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181454 5'
12392	24552	30907	2.2	2.3E-02	U939394.1	NT	Streptomyces sp. alpha-1,3/4-lucosidase precursor gene, complete cds
12447	25100		3.04	2.3E-02	U11077.1	NT	Dictyostellum discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds
12660	24940		1.73	2.3E-02	11426388	NT	Homo sapiens dead ringer (Drosophila)-like 1 (DRIL1), mRNA
767	13386	25885	3	2.2E-02	AF018267.1	NT	Columbia livia nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1783	14373		1.03	2.2E-02	4557448	NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
2059	14639	27212	1.33	2.2E-02	Z82001.1	NT	S. pneumoniae pcpA gene and open reading frames
3482	16088		2.1	2.2E-02	AA577785.1	EST_HUMAN	nt24404.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3'
3708	16309		3.58	2.2E-02	AF083094.1	NT	Infectious bursal disease virus segment B strain L4 VP1 gene, complete cds
3820	16518	28984	1.11	2.2E-02	AW601317.1	EST_HUMAN	PMO-BT0340-170100-004-b03 BT0340 Homo sapiens cDNA
3992	16590	29062	0.85	2.2E-02	Z74283.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL245c
5225	17780	30209	0.92	2.2E-02	Z73597.1	NT	S. cerevisiae chromosome XVI reading frame ORF YPL241c
7294	19822	32881	3.52	2.2E-02	AV699721.1	EST_HUMAN	AV699721 GKB Homo sapiens cDNA clone GKBAND03 3'
8312	20853	33778	2.56	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8312	20853	33779	2.56	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8744	21283	34205	0.75	2.2E-02	X79468.1	NT	P. vulgaris alpha tub 2 mRNA
9574	22074	35036	0.57	2.2E-02	AJ243025.1	NT	Mus musculus partial FBPhase 2 gene for Fructose-1,6-bisphosphatase, exon 5 and intron 5
9574	22074	35037	0.57	2.2E-02	AJ243025.1	NT	Mus musculus partial FBPhase 2 gene for Fructose-1,6-bisphosphatase, exon 5 and intron 5
9604	22104	35066	1.88	2.2E-02	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9604	22104	35067	1.88	2.2E-02	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10106	22601		0.86	2.2E-02	6678140	NT	Mus musculus Sjogren syndrome antigen A1 (Ssa1), mRNA
12120	24379		3.95	2.2E-02	AA503553.1	EST_HUMAN	ne47h07.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:900541 3' similar to contains Alu repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
444	13077		4.45	2.1E-02	AV761502.1	EST_HUMAN	AV761502 MDS Homo sapiens cDNA clone MDSADG01 5'
474	13107		5.21	2.1E-02	AF028726.1	NT	Dicotyledon discoidium histidine kinase C (dhkC) mRNA, complete cds
1308	13900	26420	8.15	2.1E-02	U72073.1	NT	Bacillus subtilis cotKLM cluster, CotK (cotK), and spore coat protein CotM (cotM) genes, complete cds
1430	14022	26550	1.46	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1430	14022	26551	1.46	2.1E-02	AF204395.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
2842	13426	25934	3.37	2.1E-02	N29266.1	EST_HUMAN	W43h07.1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:284541 5'
3184	14680	27231	0.93	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-111 BT0546 Homo sapiens cDNA
3184	14680	27232	0.93	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-111 BT0546 Homo sapiens cDNA
3943	16246	26721	1.47	2.1E-02	AA461271.1	EST_HUMAN	zx63b09.1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone IMAGE:796121 5'
4211	16800	26249	0.77	2.1E-02	Z74293.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL245c
4398	16983	29426	0.83	2.1E-02	BF343655.1	EST_HUMAN	602015306F1 NC1 CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4151161 5'
4540	17124	29568	1.84	2.1E-02	U44914.1	NT	Borrelia burgdorferi plasmid cp32.2, erpC and erpD genes, complete cds; and unknown genes
4552	17135	29583	1.3	2.1E-02	A1768127.1	EST_HUMAN	wg81d11.xt Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3'
4820	17398	29852	5.95	2.1E-02	Y08601.1	NT	A.thaliana mitochondrial genome, part A
4836	17414	29867	0.57	2.1E-02	AA66573.1	EST_HUMAN	eg55g12.s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126918 3'
4944	17519	29867	0.83	2.1E-02	A1823432.1	EST_HUMAN	wh54905.x1 NC1 CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2384528 3'
5321	17883		1.52	2.1E-02	S62470.1	NT	BB1=malignant cell expression-enhanced gene/tumor progression-enhanced gene (human, UM-UC-9 bladder carcinoma cell line, mRNA, 1897 nt)
5821	18445	31167	0.8	2.1E-02	AW379526.1	EST_HUMAN	GM4-HT0244-111199-040-R03 HT0244 Homo sapiens cDNA
7128	19466	32284	0.74	2.1E-02	BF086799.1	EST_HUMAN	QV3-GN0058-120900-329-a12 GN0058 Homo sapiens cDNA
8458	20896	33914	0.66	2.1E-02	9790238	NT	Mus musculus sorting nexin 1 (Snx1), mRNA
8422	21831	34879	0.58	2.1E-02	AA984288.1	EST_HUMAN	am83e07.s1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains
9549	22049	35010	2.41	2.1E-02	AJ243213.1	NT	Alu repetitive element; contains element MER11 repetitive element;
9549	22049	35011	2.41	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9894	22391	35368	1.22	2.1E-02	L29324.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9873	22408	35452	0.57	2.1E-02	AA984288.1	EST_HUMAN	Streptococcus pneumoniae integrase, excisionase, repressor protein, relaxase, UmuC MucB homolog, and
12089	18030		11.53	2.1E-02	Y19213.1	NT	am83e07.s1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains
12141	24839	30798	1.31	2.1E-02	L34170.1	NT	Alu repetitive element; contains element MER11 repetitive element;
12552	24655	30871	16.83	2.1E-02	AF183913.1	NT	Homo sapiens putative psfHbA pseudogene for hair keratin, exons 2 to 7
						NT	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
						NT	Azospirillum brasilense major outer membrane protein OmsA precursor (omsA) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
20	12699	25155	1.34	2.0E-02	BF002932.1	EST_HUMAN	7g51c08.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3309988 3' similar to contains MER1.13
21	12700	25156	9.6	2.0E-02	AW895565.1	EST_HUMAN	MER1 repetitive element;
280	12837	25422	2.31	2.0E-02	6753635	NT	QV4-NN0038-270400-187-105 NN0038 Homo sapiens cDNA
317	12971	25480	2.42	2.0E-02	AA456538.1	EST_HUMAN	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
831	13448	25955	1.2	2.0E-02	6753635	NT	aa15b10.r1 Soares_NhrMMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
1128	13729	26240	1.32	2.0E-02	AL096805.1	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
1241	13839	26356	0.79	2.0E-02	8922391	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 1(p36.33) of Homo sapiens
1241	13839	26357	0.79	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1914	14499	27053	2.3	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
1914	14499	27054	2.3	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2824	15378		3.19	2.0E-02	AL161532.2	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
3115	12699	25155	1.84	2.0E-02	BF002932.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3178	15791		1.38	2.0E-02	7305474	NT	7g51c08.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:3309988 3' similar to contains MER1.13
3284	15876		1.57	2.0E-02	AF095598.1	NT	MER1 repetitive element;
4078	16874	29135	1.54	2.0E-02	M18095.1	NT	Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B (Sema6b), mRNA
5288	17830	30255	1.12	2.0E-02	AF189368.1	NT	Arabidopsis thaliana C2H2 zinc finger protein FZF mRNA, complete cds
6056	18673	31414	0.87	2.0E-02	L35321.2	NT	P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
7553	20072	32947	1.26	2.0E-02	AP000004.1	NT	Ajellomyces capsulatus catalase isozyme A (CATA) mRNA, complete cds
7553	20072	32948	1.26	2.0E-02	AP000004.1	NT	Dictyostelium discoideum class VII unconventional myosin (myoI) gene, complete cds
9791	22289		2.5	2.0E-02	U70408.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-894000 nt. position (4/7)
10284	22759	35748	1.63	2.0E-02	AI040342.1	EST_HUMAN	Pyrococcus horikoshii OT3 genomic DNA, 777001-894000 nt. position (4/7)
10522	23080	36070	2.05	2.0E-02	Z73986.1	NT	Japanese encephalitis virus envelope protein mRNA, partial cds
11250	23780	36836	2.85	2.0E-02	D68184.1	NT	wa17b02.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2298315 3'
11500	23978	37047	1.58	2.0E-02	10947055	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 93/162
11530	23978	37048	1.58	2.0E-02	10947055	NT	Equus caballus DNA for 17alpha-hydroxylase/17,20-lyase, complete cds
11654	18034	30494	1.91	2.0E-02	AA456538.1	EST_HUMAN	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
12138	15376		1.94	2.0E-02	AL161532.2	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
12635	24711		8.4	2.0E-02	T60037.1	EST_HUMAN	aa15b10.r1 Soares_NhrMMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
722	13342	25832	1.93	1.9E-02	AA572764.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
							jd04c09.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24875 5'
							nf19a07.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:914196 similar to contains L1 t1 L1
							repetitive element;

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1658	14251	26785	0.96	1.9E-02	P18488	SWISSPROT	EMPTY SPIRACLES HOMEOTIC PROTEIN
2083	14864	27234	1.96	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2083	14864	27235	1.96	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2549	15113	27883	0.9	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
2930	15546	28021	8.7	1.9E-02	AA713858.1	EST_HUMAN	hw04105.s1 NCLCGAP_SS1 Homo sapiens cDNA clone IMAGE:1238337 3'
2980	15598	28076	1.56	1.9E-02	AV648669.1	EST_HUMAN	AV648669 GLC Homo sapiens cDNA clone GLCBLH07 3'
3298	15809		0.75	1.9E-02	AB033611.1	NT	Utrichus talpoides mitochondrial gene for cytochrome b, complete cds
3671	16272		1.09	1.9E-02	N52250.1	EST_HUMAN	y228b02.s1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:284331 3'
3768	16367		6.81	1.9E-02	BE738088.1	EST_HUMAN	Myocaplasma imitans VihA1 precursor (vihA1) and VihA2 precursor (vihA2) genes, partial cds
4121	16714	29170	1.48	1.9E-02	AF141940.1	NT	HOMEOTIC BICOID PROTEIN (PRD-4)
4271	16857	29305	1.57	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4271	16857	29306	1.57	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4639	17221	29675	3.21	1.9E-02	A1452989.1	EST_HUMAN	h46404.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element;
5157	15113	27883	2.73	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5519	18151	30965	0.83	1.9E-02	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
5660	18287	30765	1.38	1.9E-02	L47572.1	NT	Meleagris gallopavo paraoxonase-2 (PON2) mRNA, complete cds
5959	18581		0.81	1.9E-02	AB019507.1	NT	Drosophila kaneko' gene for glycerol-3-phosphate dehydrogenase, complete cds
7158	19880	32534	1.41	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
7158	19890	32535	1.41	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
8508	21045		1.06	1.9E-02	AL162754.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome, segment 3/7
9254	21780	34732	0.94	1.9E-02	BF316129.1	EST_HUMAN	601856130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125482 5'
9828	22128	35093	0.88	1.9E-02	L10114.1	NT	Nicotiana tabacum type II phytochrome (phyB) gene, complete cds
9958	22453	35435	1.04	1.9E-02	BF695832.1	EST_HUMAN	601852385F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4078253 5'
10054	22549	35543	0.49	1.9E-02	N39160.1	EST_HUMAN	yy49H08.s1 Soares multiple sclerosis 2NBHMSHP Homo sapiens cDNA clone IMAGE:276639 3'
10151	22846	35639	0.56	1.9E-02	D64001.1	NT	Synechocystis sp. PCC6803 complete genome, 20/27, 2539000-2844794
11878	24847	30801	4.29	1.9E-02	AF101065.1	NT	Hirudo medicinalis intermediate filament glierin mRNA, complete cds
12477	24818		1.27	1.9E-02	L11068.1	NT	Candida albicans lambda Ca3/B fragment
12567	24980	30878	1.7	1.9E-02	X68271.1	NT	H.sapiens MUC18 gene exon 16
368	13017	25500	1.84	1.9E-02	AW771104.1	EST_HUMAN	hns206.x1 NCLCGAP_Cot17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element MER26 repetitive element;
714	13335	25821	2.26	1.9E-02	BF308122.1	EST_HUMAN	601884329F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139883 5'
1202	13802	26315	1.51	1.9E-02	X17684.1	NT	H.francisci mRNA for myelin basic protein (MBP)
1484	14077	26615	2.3	1.9E-02	AF243382.1	NT	Drosophila melanogaster cytoplasmic protein encore (enc) mRNA, complete cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2704	15261	27828	1.22	1.8E-02	AE004544.1	NT	Pseudomonas aeruginosa PA01, section 105 of 528 of the complete genome
3247	15859		0.72	1.8E-02	AI805829.1	EST_HUMAN	U52809.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090296 3'
3956	16554	29023	1.07	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
3956	16554	29024	1.07	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
4160	16752		1.41	1.8E-02	AA861446.1	EST_HUMAN	ak2404.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406935 3'
4521	17105	29551	1.67	1.8E-02	AW936363.1	EST_HUMAN	QV4-DT0021-301268-071-b11 DT0021 Homo sapiens cDNA
5090	17663	30103	1.06	1.8E-02	OB0810	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.2
6901	19635	32473	4.27	1.8E-02	P14310	SWISSPROT	HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5REGION
8071	20613	33527	0.81	1.8E-02	U37091.1	NT	Mus musculus carbonic anhydrase IV gene, complete cds
8404	20944	33866	0.91	1.8E-02	AW905327.1	EST_HUMAN	QV2-NN1073-220400-159-109 NN1073 Homo sapiens cDNA
8449	20989	33907	0.75	1.8E-02	6678943	NT	Mus musculus microtubule-associated protein 2 (Map2), mRNA
9413	21922	34870	0.45	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9413	21922	34871	0.45	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9560	22060		2.41	1.8E-02	AA897543.1	EST_HUMAN	aj9208.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394921 3' similar to gb.L11672 ZINC FINGER PROTEIN 91 (HUMAN);
9975	22470	35453	1.72	1.8E-02	BE778274.1	EST_HUMAN	601463545F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866983 5'
10126	22621	35611	1.12	1.8E-02	X98933.1	NT	L. stagnalis mRNA for myomodulin neuropeptide precursor
11313	23011	36019	1.79	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11313	23011	36020	1.79	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11480	23930	37001	1.73	1.8E-02	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt, position (6/7)
11489	23938	37008	3.88	1.8E-02	U62749.1	NT	Zea mays acidic ribosomal protein P2a-3 (pp2a-3) mRNA, partial cds
939	13552	26068	0.77	1.7E-02	BE394889.1	EST_HUMAN	601310626F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632180 5'
1827	14416	26963	1.89	1.7E-02	AW573183.1	EST_HUMAN	h164a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.11 L1 repetitive element
1827	14416	26964	1.89	1.7E-02	AW573183.1	EST_HUMAN	h164a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.11 L1 repetitive element
1912	14497		3.27	1.7E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2159	14736		12.81	1.7E-02	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitsugumin28, complete cds
2332	14903	27474	4.64	1.7E-02	S74186.1	NT	[microsatellite INRA41] [Ovis aries=sheep, Genomic, 361 nt, segment 1 of 2]
3028	15644	28123	0.84	1.7E-02	AI147615.1	EST_HUMAN	qb22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696982 3'
3562	16166		4.33	1.7E-02	AW827968.1	EST_HUMAN	hm45a04.x1 NCI_CGAP_RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains MER19.b1 MER19 repetitive element
3687	16288		0.65	1.7E-02	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4248	16836		1.08	1.7E-02	AA669818.1	EST_HUMAN	act19f04.s1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:859827 3' similar to contains Alu repetitive element/contains element MER24 repetitive element;
4278	16864		2.52	1.7E-02	RO2506.1	EST_HUMAN	ye86f08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124647 5'
4551	17134	28582	0.81	1.7E-02	AI305279.1	EST_HUMAN	qmo8g07.x1 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1881276 3' similar to gb:X52359 ZINC FINGER PROTEIN 30 (HUMAN);
4626	17209	29659	1.44	1.7E-02	AW573183.1	EST_HUMAN	hf34a03.x1 Soares NFL T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.1 L1 repetitive element;
4824	17402	29855	1.78	1.7E-02	V00841.1	NT	Messenger RNA for anglerfish (Lophius americanus) somatostatin II
4836	17511		5.59	1.7E-02	AI015076.1	EST_HUMAN	ov51602.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1640858 3'
8274	18882	31650	1.8	1.7E-02	A1769247.1	EST_HUMAN	wg35f09.x1 Soares NSF_F8_PW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367113 3' similar to contains Alu repetitive element;
8693	19289	32091	1.98	1.7E-02	AI038280.1	EST_HUMAN	oy85f03.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672681 3'
7112	19452	32268	1.05	1.7E-02	AF190930.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
7255	19783	32639	1.96	1.7E-02	8400718	NT	Homo sapiens nebulin (NEB), mRNA
7394	19919	32783	1.07	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
7724	19918	32784	1.07	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
7724	20232		1.7	1.7E-02	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-50
9357	20298	33195	0.87	1.7E-02	U21854.1	NT	Caenorhabditis elegans cCAF1 protein gene, complete cds
8615	22115	35079	1.31	1.7E-02	AL040554.1	EST_HUMAN	DKFZp4340314.1_1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp4340314 5'
12462	25025	30619	3.35	1.7E-02	AW803482.1	EST_HUMAN	CM4-NN1030-0400-130-f08 NN1030 Homo sapiens cDNA
537	13188		3.38	1.6E-02	AL021929.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 13/162
1696	14289	28825	1.05	1.6E-02	Y18889.1	NT	Treponema maltophilum flaB2, flaB3 and flhD genes for flagellin subunit proteins and CAP protein homologue
2290	14884	27438	2.13	1.6E-02	Q84178	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2290	14884	27438	2.13	1.6E-02	Q84178	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2600	15182	27730	0.98	1.6E-02	AJ006345.1	NT	Homo sapiens KVLQT1 gene
2669	15227	27799	1.82	1.6E-02	AA484872.1	EST_HUMAN	ne81d08.s1 NCI CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910667
2716	15275		1.14	1.6E-02	AB014534.1	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
3052	15688	28146	0.73	1.6E-02	AF112282.1	NT	Lasaea sp. isolate IBd cytochrome oxidase III gene, partial cds; mitochondrial gene for mitochondrial product
3578	16182	28664	5.61	1.6E-02	AW850652.1	EST_HUMAN	IL3-CT0219-180200-063-C07 CT0219 Homo sapiens cDNA
3814	16512	28974	0.62	1.6E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4254	16942		1.77	1.6E-02	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RaGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
4388	16974	29424	1.26	1.6E-02	AW875407.1	EST_HUMAN	QV2-PT0012-140100-030-107 PT0012 Homo sapiens cDNA
4901	17478	29632	3.99	1.6E-02	AI769132.1	EST_HUMAN	wg34b09.x1 Soares NSF_F8_9W_OI_PA_P_S1 Homo sapiens cDNA clone IMAGE:2366869 3'
5306	17968		0.61	1.6E-02	N80156.1	EST_HUMAN	za65e07.s1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:297444 3'
5807	18432	31153	1.26	1.6E-02	8871715	NT	Mus musculus CD5 antigen (Cd5), mRNA
6752	19346	32152	2	1.6E-02	AB015281.1	NT	Candida albicans CaGCR3 gene, complete cds
7011	19509	32328	1.22	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7011	19509	32330	1.22	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7696	20205	33092	0.9	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8064	20606	33518	0.78	1.6E-02	AJ277662.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
8119	20680		1.55	1.6E-02	X05151.1	NT	Human apoC-II gene for preproapolipoprotein C-II
9953	22448		2.32	1.6E-02	AF079764.1	NT	Drosophila melanogaster enhancer of polycomb (E(Pc)) mRNA, complete cds
10317	22811	35805	1.17	1.6E-02	AA572818.1	EST_HUMAN	nf19g03.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT
10317	22811	35806	1.17	1.6E-02	AA572818.1	EST_HUMAN	nf19g03.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT
10788	24800	36319	2.38	1.6E-02	Z94928.1	NT	P29294 TELOKIN. [1]:
11090	23602	36840	2.5	1.6E-02	AL161508.2	NT	G.gallus microsatellite DNA (LE10260 (=T1611E11))
11090	23602	36841	2.5	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11385	23937	36899	2.38	1.6E-02	AI373558.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11855	14864	27438	3.63	1.6E-02	Q64176	SWISSPROT	qz96e10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:2042442 3'
11855	14864	27439	3.63	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
781	13400		51.07	1.5E-02	8923734	NT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2187	14763	27332	4.36	1.5E-02	N39521.1	EST_HUMAN	Homo sapiens transcription factor (HSA130894), mRNA
2219	14794	27367	1.76	1.5E-02	AL161594.2	NT	w27b07.s1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:243925 3'
3097	15712	28183	0.99	1.5E-02	AJ006216.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
3097	15712	28184	0.99	1.5E-02	AJ006216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3787	16387	28853	0.96	1.5E-02	BF082942.1	EST_HUMAN	Homo sapiens CACNA1F gene, exons 1 to 48
4222	16810	29257	0.86	1.5E-02	AA160967.1	EST_HUMAN	MR4-TN0115-080900-201-b12 TN0115 Homo sapiens cDNA
5190	17728		0.78	1.5E-02	MT3878.1	NT	zq40g10.r1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632226 5'
5405	17963	30374	1.14	1.5E-02	AW770341.1	EST_HUMAN	Human interleukin 2 gene, exons 1 and 2

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6436	19039	31826	1.31	1.5E-02	Q09711	SWISSPROT	HYPOTHETICAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME 1
7360	19886		1.62	1.5E-02	11487282	NT	Cyanophora paradoxa cyanelle, complete genome
7432	19956	32821	1.36	1.5E-02	11418713	NT	Homo sapiens KIAA1009 protein (KIAA1009), mRNA
7815	20358	33265	1.44	1.5E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7822	20364	33273	4.16	1.5E-02	11417739	NT	Homo sapiens velyl-rRNA synthetase 2 (VARS2), mRNA
8764	21303	34224	1.62	1.5E-02	BF345554.1	EST_HUMAN	802019135F1 NCL_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4154504 5'
9389	21812		0.51	1.5E-02	AF096774.1	NT	Homo sapiens kinase-related protein isoform 1 mRNA, complete cds
9490	21948	34895	1.64	1.5E-02	D44606.1	NT	Saccharomyces cerevisiae chromosome VI plasmid GapC
9725	22223	35199	1.08	1.5E-02	R32667.1	EST_HUMAN	yh54b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
9725	22223	35200	1.08	1.5E-02	R32667.1	EST_HUMAN	yh54b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
10897	23227		1.71	1.5E-02	D26547.1	NT	Rice gene for thioridoxin h, complete cds
11047	23560	36597	2.32	1.5E-02	L40609.1	NT	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's
12076	24892		2.25	1.5E-02	AW750834.1	EST_HUMAN	RC4-CN0049-140100-011-011 CN0049 Homo sapiens cDNA
12638	24712		1.55	1.5E-02	AI763127.1	EST_HUMAN	wf06h03.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389493 3' similar to contains Alu repetitive element; contains element MER28 MSR1 repetitive element ;
442	13075		1.41	1.4E-02	AE002230.2	NT	Chlamydomonas reinhardtii AR39, section 58 of 94 of the complete genome
1157	13760	26270	4.22	1.4E-02	7705980	NT	Homo sapiens NESH protein (LOC51225), mRNA
1289	13883		1.29	1.4E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1341	13936		3.36	1.4E-02	U67779.1	NT	Xenopus laevis neurogenin related 1b (X-NGNR-1b) mRNA, complete cds
1564	14156		1.08	1.4E-02	AV723785.1	EST_HUMAN	AV723785 HTB Homo sapiens cDNA clone HTBAHH11 5'
3249	15861	28342	1.91	1.4E-02	AF160969.2	NT	Bifidobacterium longum Na+/H+ antiporter (nhaS), cytosine deaminase and alpha-galactosidase (eglL) genes, complete cds; and N-acetylglucosamine/xylose repressor protein (nagC/xyR) gene, partial cds
3445	16053	28530	0.96	1.4E-02	AW074212.1	EST_HUMAN	xb09d09.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575793 3'
3531	16138	28616	5.67	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3531	16138	28617	5.67	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3571	16175	28657	0.68	1.4E-02	4503628	NT	Homo sapiens coagulation factor XII (Hageman factor) (F12), mRNA
3717	16318	28786	6.27	1.4E-02	6896918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-B), mRNA
4587	17170	29614	8.66	1.4E-02	AW962688.1	EST_HUMAN	EST1374761 IMAGE resequences, MAGG Homo sapiens cDNA
4587	17170	29615	8.66	1.4E-02	AW962688.1	EST_HUMAN	EST1374761 IMAGE resequences, MAGG Homo sapiens cDNA
4767	17348	29787	1.2	1.4E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4767	17348	29788	1.2	1.4E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
5003	17576	30020	6.64	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5003	17576	30021	6.64	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
6547	19145	31941	4.61	1.4E-02	AA559030.1	EST_HUMAN	nt11c04.s1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029980 3' similar to contains Alu repetitive element;
6547	19145	31942	4.61	1.4E-02	AA559030.1	EST_HUMAN	nt11c04.s1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1029980 3' similar to contains Alu repetitive element;
8081	20623		1.97	1.4E-02	AL022073.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 88/162
8828	21368	34292	1.24	1.4E-02	M81702.1	NT	Candida boidinii methanol oxidase (AOD1) gene, complete cds
9082	21818	34553	0.99	1.4E-02	ALJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
9321	21835	34786	2.48	1.4E-02	BE544561.1	EST_HUMAN	601078239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3484241 5'
10451	22845		0.81	1.4E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11765	24156	36772	12.79	1.4E-02	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
12134	24387		3.82	1.4E-02	AF324985.1	NT	Arabidopsis thaliana F21J9.2 mRNA, complete cds
12433	24574		2.32	1.4E-02	11426968	NT	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA
1905	14490		1.18	1.3E-02	BE739263.1	EST_HUMAN	601556462F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828335 5'
1998	14580	27138	2.55	1.3E-02	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3250	15862	28343	1.91	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3250	15862	28344	1.91	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
4041	16639		1.66	1.3E-02	AF169288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds
5455	18090	30447	1.46	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxq28orf
5455	18090	30448	1.46	1.3E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mmxq28orf
6312	18919	31694	1.4	1.3E-02	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
6345	18951	31728	0.96	1.3E-02	M62962.1	NT	C.reinhardtii ribulose 1,5-bisphosphate carboxylase/oxygenase activase mRNA, complete cds
7041	18061	30449	1.25	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48
7041	18061	30450	1.25	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7578	20094	32971	4.79	1.3E-02	AL031593.1	EST_HUMAN	ow06g05.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element;
8418	20958	33876	1.63	1.3E-02	AF156961.1	NT	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
10108	22803	35593	1.71	1.3E-02	M63707.1	NT	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
10178	22873	35665	0.77	1.3E-02	AE001304.1	NT	Chlamydia trachomatis section 31 of 87 of the complete genome
10871	23392	36406	4.07	1.3E-02	AW268563.1	EST_HUMAN	xx344603.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
10871	23392	36407	4.07	1.3E-02	AW268563.1	EST_HUMAN	xx344603.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11742	26051		2.12	1.3E-02	X51780.1	NT	Yeast ABP1 gene for actin binding protein
12139	25039		2	1.3E-02	Z69117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870
12248	24457		2.77	1.3E-02	9833069	NT	Human herpesvirus 6B, complete genome
12438	24813		47.13	1.3E-02	AF152238.1	NT	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
228	12888		20.25	1.2E-02	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
377	13025	25511	3.79	1.2E-02	AA059299.1	EST_HUMAN	Zf65g01.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element
478	13111	25601	1.71	1.2E-02	P38898	SWISSPROT	L1 repetitive element ;
768	13387	25886	8.37	1.2E-02	AI183522.1	EST_HUMAN	HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION
2221	14798	27389	1.85	1.2E-02	AL163213.2	NT	qtd86a12.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.11 L1 repetitive element ;
2223	14798	27371	1.15	1.2E-02	AV731704.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C013
2487	15052	27624	1	1.2E-02	AW172350.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
2542	15106	27678	1.05	1.2E-02	BE538310.1	EST_HUMAN	x37e09.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
3135	15749	28413	7.56	1.2E-02	AA075418.1	EST_HUMAN	601068406F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5'
3327	15937	28413	2.02	1.2E-02	R92805.1	EST_HUMAN	601068406F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5'
4938	17513	29859	0.61	1.2E-02	AL161593.2	NT	znr8e03.11 Stralagene ovarian cancer (#637219) Homo sapiens cDNA clone IMAGE:545020 5'
5040	17613	30057	2.65	1.2E-02	U91328.1	NT	y11b08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
5194	17759		1.61	1.2E-02	AB019786.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 89
5244	17808	30230	2.01	1.2E-02	AV731704.1	EST_HUMAN	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP T3) gene, complete cds
5927	18549	31275	1.76	1.2E-02	D78569.1	NT	Cynops pyrrhogaster Cpb1q1T mRNA, partial cds
7078	19650	32489	5.21	1.2E-02	AF175412.1	NT	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
7334	19861	32725	1.08	1.2E-02	H02197.1	EST_HUMAN	Rana rugosa mRNA for calreticulin, complete cds
7353	19879	32744	19.46	1.2E-02	AV732093.1	EST_HUMAN	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
7939	20481	33392	2.3	1.2E-02	Q11205	SWISSPROT	x34h112.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150695 3'
8133	20674	33585	1.2	1.2E-02	AF193612.1	NT	AV732093 HTF Homo sapiens cDNA clone HTFBJC09 5'
8133	20674	33588	1.2	1.2E-02	AF193612.1	NT	CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NAc6S) (GAL-BETA-1,3-GALNAc-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GAL4.2) (SIAT4-B)
8822	21361		1.06	1.2E-02	IT6987.1	EST_HUMAN	Homo sapiens fringe protein mRNA, partial cds
							Homo sapiens fringe protein mRNA, partial cds
							yd72c08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113774 3'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9557	22057	35018	2.7	1.2E-02	AB031013.1	NT	Norwalk-like virus genogroup 2 gene for capsid protein, complete cds
9559	22089	35053	1.74	1.2E-02	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
12446	24582		4.73	1.2E-02	C18119.1	EST_HUMAN	C18119 Human placenta cDNA (TFujwara) Homo sapiens cDNA clone GEN-557G06 5'
1312	13906	26428	1.49	1.1E-02	AA070364.1	EST_HUMAN	zm69a11.s1 Stratagene neuroepithelium (R937231) Homo sapiens cDNA clone IMAGE:530924 3'
1744	14334	26880	1.91	1.1E-02	X75491.1	NT	H sapiens LIPA gene, exon 4
1744	14334	26881	1.91	1.1E-02	X75491.1	NT	H sapiens LIPA gene, exon 4
2082	14663	27233	5.42	1.1E-02	BF345263.1	EST_HUMAN	602018037F1 NCL_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4153808 5'
2902	15519		4.2	1.1E-02	N99523.1	EST_HUMAN	za40e05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295040 5'
3575	16179	28662	2.86	1.1E-02	AI653508.1	EST_HUMAN	ta95b10.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW:XP_F_HUMAN
4094	16689		2.1	1.1E-02	BE144637.1	EST_HUMAN	Q82889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL;
4183	16773		0.61	1.1E-02	AW813796.1	EST_HUMAN	PM3-HT0175-300999-001-h06 HT0175 Homo sapiens cDNA
4956	17531	29973	2.09	1.1E-02	AL048383.2	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
							DKFZp586E0824_s1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586E0924
6298	18906	31677	1.03	1.1E-02	U68480.1	NT	Bacillus subtilis SpoVK (spvK), YnaA (ynbA), YnaB (ynbB), GlnR (glnR), glutamine synthetase (glnA), YnaA (ynbA), YnaB (ynbB), YnaC (ynbC), YnaD (ynbD), YnaE (ynbE), YnaF (ynbF), YnaG (ynbG), YnaH (ynbH), YnaI (ynbI), YnaJ (ynbJ), xylan beta-1,4-xylosyl>
7594	20108	32983	2.55	1.1E-02	BE149611.1	EST_HUMAN	RC1-HT0256-100300-016-h07 HT0256 Homo sapiens cDNA
8199	20740	33652	0.49	1.1E-02	P80394	SWISSPROT	METALLOTHIONEIN (MT-1/MT-2)
8199	20740	33653	0.49	1.1E-02	P80394	SWISSPROT	METALLOTHIONEIN (MT-1/MT-2)
8574	21113	34032	0.64	1.1E-02	AW996160.1	EST_HUMAN	QV3-BN0045-220300-128-h02 BN0045 Homo sapiens cDNA
8756	21295	34215	0.69	1.1E-02	C04803.1	EST_HUMAN	C04803 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone 3NHC4040
8833	21372	34297	7.39	1.1E-02	Q61982	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
9842	22340	35322	2.07	1.1E-02	AA082578.1	EST_HUMAN	zn24a01.r1 Stratagene neuroepithelium NT2RAMI 837234 Homo sapiens cDNA clone IMAGE:548328 5'
10006	22501	35492	3.79	1.1E-02	AA314665.1	EST_HUMAN	EST186494 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
10858	23379	36398	3.88	1.1E-02	11435505	NT	Homo sapiens T-box 5 (TBX5), mRNA
11702	24115		2.57	1.1E-02	AA688239.1	EST_HUMAN	ab7711.1 s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains
12512	16773		1.87	1.1E-02	AW813796.1	EST_HUMAN	Alu repetitive element
7	12896	25144	6.97	1.0E-02	AW846120.1	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
1570	14163	26694	2.33	1.0E-02	AW368126.1	EST_HUMAN	MR3-CT0176-111099-003-e10 CT0176 Homo sapiens cDNA
2606	15188		1.9	1.0E-02	AA806389.1	EST_HUMAN	CM2-HT0177-041099-017-h12 HT0177 Homo sapiens cDNA
3126	15740	28209	3.7	1.0E-02	BE835556.1	EST_HUMAN	oc22h08.s1 NCL_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1350495 3'
3302	15913	28391	1.41	1.0E-02	BE968999.1	EST_HUMAN	RC0-FN0025-250500-021-d02 FN0025 Homo sapiens cDNA
							601649967R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933689 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3558	16162		0.83	1.0E-02	AW845621.1	EST_HUMAN	MRO-CT0060-081098-003-110 CT0060 Homo sapiens cDNA
3650	16548	29016	0.88	1.0E-02	AI065086.1	EST_HUMAN	HIA0921 Human fetal liver cDNA library Homo sapiens cDNA
4891	17466	29921	5.12	1.0E-02	6753521	NT	Mus musculus corticotropin releasing hormone receptor 2 (Chr2), mRNA
4970	17544	29886	5.03	1.0E-02	R96567.1	EST_HUMAN	Mus musculus corticotropin releasing hormone receptor 2 (Chr2), mRNA
5221	17786	30204	1.01	1.0E-02	AF218910.1	NT	Yq54h01.1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:198633 5'
5317	17878	30298	0.88	1.0E-02	P06599	SWISSPROT	Homo sapiens attractin precursor (ATRN) gene, exon 25 and complete cds, alternatively spliced
5394	17952		16.85	1.0E-02	AV723678.1	EST_HUMAN	EXTENSIN PRECURSOR
5445	18000		3.87	1.0E-02	D34632.1	NT	AV723678 HTB Homo sapiens cDNA clone HTBAPF08 5'
5610	18239	30888	0.8	1.0E-02	H52681.1	EST_HUMAN	Arabidopsis thaliana acc2 gene for acetyl-CoA carboxylase, partial cds
5921	18543	31269	0.7	1.0E-02	AF309388.1	NT	YJ36H11.1 Soares ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:235941 5'
6284	18872	31642	0.99	1.0E-02	AF257303.1	NT	Mus musculus transcription complex subunit NF-ATc4 (Nfatc4) gene, exons 1 and 2
6328	18934	31709	2.87	1.0E-02	AW577113.1	EST_HUMAN	Mus musculus synaptotagmin II (Syn2) gene, complete cds
6328	18934	31710	2.67	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-H01 BT0356 Homo sapiens cDNA
6859	19593	32425	2.22	1.0E-02	Z29642.1	NT	MR4-BT0356-070100-201-H01 BT0356 Homo sapiens cDNA
8240	20761		0.46	1.0E-02	Z28107.1	NT	Z.mays U3snRNA pseudogene
9314	21828	34778	4.26	1.0E-02	BF036331.1	EST_HUMAN	S.cerevisiae chromosome XI reading frame ORF YKL107w
9314	21828	34779	4.29	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
11143	23651		2.17	1.0E-02	AF157559.1	NT	601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
11246	23776	36833	2.02	1.0E-02	AV760016.1	EST_HUMAN	Citridia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds, mitochondrial gene for mitochondrial product
11785	25110		2.16	1.0E-02	Q62203	SWISSPROT	AV760016 MDS Homo sapiens cDNA clone MDSBDC10 5'
11847	24862	30705	4.64	1.0E-02	AW935521.1	EST_HUMAN	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
11881	24922		6.07	1.0E-02	S70330.1	NT	RC2-DT0007-120200-016-h02 DT0007 Homo sapiens cDNA
12254	24898		1.53	1.0E-02	AJ276505.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
12422	24892		4.42	1.0E-02	X62854.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
926	13539	26057	3.16	9.0E-03	AI798126.1	EST_HUMAN	H.sapiens gene for Me491/CD63 antigen
1307	13901		1.26	9.0E-03	BE781889.1	EST_HUMAN	wh4209.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element
2439	15006	27578	3.82	9.0E-03	AL161559.2	NT	MER22 MER22 repetitive element
2449	15016	27599	0.87	9.0E-03	AF096934.1	NT	601470242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873346 5'
2931	15547	28022	0.61	9.0E-03	AI251744.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
2931	15547	28023	0.61	9.0E-03	AI251744.1	EST_HUMAN	Mus musculus MHC class III protein RP1 (Rp1) mRNA, partial cds
3731	16332	28798	0.8	9.0E-03	J05184.1	NT	qh90f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
5978	18598		1.17	9.0E-03	AI809792.1	EST_HUMAN	qh90f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'

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6741	19335		4.24	9.0E-03	BE745988.1	EST_HUMAN	601573438F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834762 5'
7487	20010	32876	0.73	9.0E-03	8922570	NT	Homo sapiens hypothetical protein FLJ10650 (FLJ10650), mRNA
7816	20359		0.83	9.0E-03	AL039991.1	EST_HUMAN	DKFZp434L0412.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L0412 5'
8191	20732		0.56	9.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
9759	22257	35240	0.5	9.0E-03	P26011	SWISSPROT	INTEGRIN BETA-7 PRECURSOR (INTEGRIN BETA-P) (M290 IEL ANTIGEN)
9776	22274	35259	1.26	9.0E-03	P20808	SWISSPROT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
10865	23386		1.8	9.0E-03	Y18000.1	NT	Homo sapiens NF2 gene
10891	23412	36431	1.71	9.0E-03	BE395380.1	EST_HUMAN	601310881F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3832181 5'
11505	23954	37022	1.58	9.0E-03	L11144.1	NT	Homo sapiens preprogalanin (GAL1) gene, exons 1, 2, and 3
11505	23954	37023	1.58	9.0E-03	L11144.1	NT	Homo sapiens preprogalanin (GAL1) gene, exons 1, 2, and 3
12001	25111		1.79	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291296-001-e09 HT0452 Homo sapiens cDNA
12221	25105		36.8	9.0E-03	BE348385.1	EST_HUMAN	hw17609.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183161 3'
12319	24508	30943	1.38	9.0E-03	AL183267.2	NT	Homo sapiens chromosome 21 segment HS21C067
12539	24649		31.67	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291296-001-e09 HT0452 Homo sapiens cDNA
527	13159		2.87	8.0E-03	AA723007.1	EST_HUMAN	zh30e03.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413596 3' similar to contains
1026	13637	26152	35.57	8.0E-03	AF106656.1	NT	Alu repetitive element;
2203	14779	27351	1.28	8.0E-03	AL183283.2	NT	Homo sapiens chromosome 21 segment HS21C063
3351	15959	28436	0.99	8.0E-03	BE171225.1	EST_HUMAN	RC1-HT0545-120200-011-b09 HT0545 Homo sapiens cDNA
3404	16013	28492	0.89	8.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3738	16339	28805	1.77	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
3738	16339	28806	1.77	8.0E-03	P32644	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4343	16930	29371	1.19	8.0E-03	BE840049.1	EST_HUMAN	QV0-FN0181-140700-304-g10 FN0181 Homo sapiens cDNA
4472	17058	29505	6.36	8.0E-03	BF363327.1	EST_HUMAN	CN4-NN0119-300800-223-b05 NN0119 Homo sapiens cDNA
5378	17937	30350	1.02	8.0E-03	U02970.1	NT	Prototheca wickerhamii 263-11 complete mitochondrial DNA
5410	17987	30376	0.88	8.0E-03	P01871	SWISSPROT	IG MU CHAIN C REGION
5714	18340	30846	2.89	8.0E-03	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RaiGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
6346	24762	31730	1.34	8.0E-03	AF000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-344000 nt. position (27)
6846	19436	32251	4.45	8.0E-03	P55577	SWISSPROT	PROBABLE PEPTIDASE Y4NA
6999	19497		1.72	8.0E-03	V01109.1	NT	Human BK virus (strain MM) genome. (Closely related to SV40.)
7259	19787	32843	1.8	8.0E-03	M17197.1	NT	A. californica (marine gastropod mollusc) neuropeptide gene (bag cell), exon 1, 5' end

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7547	20097		1.84	8.0E-03	AB038287.1	NT	TuSlops truncatus mRNA for p40-phox, complete cds
8816	21355	34279	0.82	8.0E-03	P98160	SWISSPROT	BASAMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
8841	21380	34304	3.73	8.0E-03	AW808692.1	EST_HUMAN	PRECURSOR (HSPG) (PERLECAN) (PLC)
8910	21448	34370	0.68	8.0E-03	9789958	NT	MR1-ST0111-11199-011-t06 ST0111 Homo sapiens cDNA
9859	22356		4.76	8.0E-03	BE096509.1	EST_HUMAN	Mus musculus fusion 2 (human) (Fus2), mRNA
10884	23385		3.01	8.0E-03	Z49652.1	NT	QV1-BT0677-040400-131-g03 BT0677 Homo sapiens cDNA
11259	23789	36845	1.97	8.0E-03	AA828817.1	EST_HUMAN	S.cerevisiae chromosome X reading frame ORF YJR152w
11259	23789	36846	1.97	8.0E-03	AA828817.1	EST_HUMAN	cd80a09.s1 NCI_CGAP_OV2 Homo sapiens cDNA clone IMAGE:1374232
11562	24009	37079	4.96	8.0E-03	AF084589.1	NT	cd80a09.s1 NCI_CGAP_OV2 Homo sapiens cDNA clone IMAGE:1374232
11713	24123		2.81	8.0E-03	ME8035.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
11781	24154		5.99	8.0E-03	AB038181.1	NT	Oryctolagus cuniculus eIF-2a kinase mRNA, complete cds
723	13343	25833	14.03	7.0E-03	AF097183.1	NT	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
723	13343	25834	14.03	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
1012	13622	26137	5.78	7.0E-03	AF243378.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
1155	13758	26288	3.21	7.0E-03	AV731712.1	EST_HUMAN	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1408	14001		1.28	7.0E-03	Q61060	SWISSPROT	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5'
1439	14032	26560	4.09	7.0E-03	AA688298.1	EST_HUMAN	FORKHEAD BOX PROTEIN D3 (HNF3/FH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE
1550	14142	26875	3.14	7.0E-03	AW303599.1	EST_HUMAN	NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2) (HFH-2)
2297	15482	27447	2.12	7.0E-03	PO4829	SWISSPROT	ab79b09.s1 Stralagene fetal retina g37202 Homo sapiens cDNA clone IMAGE:853145 3'
3614	16217	28696	0.58	7.0E-03	A1150273.1	EST_HUMAN	xx21b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'
3830	16430	28892	0.91	7.0E-03	AW444463.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3885	16483	28945	1.01	7.0E-03	AF196344.1	NT	gf34h02.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1751855 3'
4091	16430	28892	0.63	7.0E-03	AW444463.1	EST_HUMAN	UL-H-B13-akb-o-10-Q-UJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
4704	17286		1.1	7.0E-03	AW630888.1	EST_HUMAN	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
5125	17697		2.08	7.0E-03	AL183278.2	NT	UL-H-B13-akb-o-10-Q-UJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2989836 5'
5985	18605		0.79	7.0E-03	H71106.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
6280	24760		5.32	7.0E-03	AW681059.1	EST_HUMAN	yr82g01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211824 5' similar to
6456	19057	31842	1.45	7.0E-03	W68251.1	EST_HUMAN	gb:X14723 CLUSTERIN PRECURSOR (HUMAN);
6658	19254	32056	2.98	7.0E-03	AA327128.1	EST_HUMAN	RC1-CT0286-050400-018-c08 CT0286 Homo sapiens cDNA
							zdc33f10.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:342475 5'
							EST30674 Cdon Homo sapiens cDNA 5' end

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6681	19277	32080	0.92	7.0E-03	BE857385.1	EST_HUMAN	7g34b10.x1 NCJ_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR:Q13387
7139	19519	32341	2.12	7.0E-03	BE928133.1	EST_HUMAN	Q13387 HYPOTHETICAL PROTEIN 364D8_2; contains TAR1.12 TAR1 repetitive element;
7529	20049	32921	5.78	7.0E-03	Z35838.1	NT	CM2-CT0478-230800-347-b11 CT0478 Homo sapiens cDNA
7529	20049	32922	5.78	7.0E-03	Z35838.1	NT	S.cerevisiae chromosome II reading frame ORF YBL077w
7789	20332	33238	0.54	7.0E-03	AJ229043.1	NT	S.cerevisiae chromosome II reading frame ORF YBL077w
7789	20332	33239	0.54	7.0E-03	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
8055	20597	33504	2.36	7.0E-03	BE175667.1	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
9318	21832		0.6	7.0E-03	AF111168.2	NT	RC5-HT0582-160300-011-D02 HT0582 Homo sapiens cDNA
9513	22013	34972	0.87	7.0E-03	N52378.1	EST_HUMAN	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
9636	22136	35101	2.48	7.0E-03	P48982	SWISSPROT	yy49c10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246066 3' similar to contains
9636	22136	35102	2.48	7.0E-03	P48982	SWISSPROT	Alu repetitive element;
10207	22702		0.99	7.0E-03	AV687379.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10381	22875		0.93	7.0E-03	AF769734.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10706	23235	36248	3.46	7.0E-03	AB008852.1	NT	AV687379 GKC Homo sapiens cDNA clone GKCAFC07 5'
10780	23304	36311	1.61	7.0E-03	AJ004862.1	NT	wc37e09.x1 NCJ_CGAP_P128 Homo sapiens cDNA clone IMAGE:2320840 3'
10780	23304	36312	1.61	7.0E-03	AJ004862.1	NT	Bos taurus mRNA for NDP52, complete cds
10930	23448		1.66	7.0E-03	AJ242804.1	NT	Homo sapiens partial MUC5B gene, exon 1-29
12273	25095		1.83	7.0E-03	H94065.1	EST_HUMAN	Homo sapiens partial MUC5B gene, exon 1-29
12281	24494		1.58	7.0E-03	BE263253.1	EST_HUMAN	Sporobolus stapianus mRNA for putative glycine and proline-rich protein
12382	24549		1.86	7.0E-03	Y17455.1	NT	yy15h01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:242833 3' similar to contains
12527	25092		1.38	7.0E-03	AL163300.2	NT	Alu repetitive element.
12664	24734		3.16	7.0E-03	AW868110.1	EST_HUMAN	601145154F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160476 5'
1283	13879	26400	10.8	6.0E-03	AW511148.1	EST_HUMAN	Homo sapiens LSFR2 gene, penultimate exon
1283	13879	26401	10.8	6.0E-03	AW511148.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
2800	15352	27921	1.82	6.0E-03	AF112374.1	NT	RCO-SN0052-110400-021-e04 SN0052 Homo sapiens cDNA
2916	15533	28004	3.54	6.0E-03	AA759135.1	EST_HUMAN	hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2810224 3' similar to
2916	15533	28005	3.54	6.0E-03	AA759135.1	EST_HUMAN	SW:PXN_HUMAN_075469 ORPHAN NUCLEAR RECEPTOR PXR ;
3283	15894		2.17	6.0E-03	H75660.1	EST_HUMAN	SW:PXN_HUMAN_075469 ORPHAN NUCLEAR RECEPTOR PXR ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3344	15954		0.79	6.0E-03	AF190338.1	NT	Notoncus sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
3429	16037	28518	1.14	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, septaplerin reductase and vasotocin genes, complete cds
3429	16037	28519	1.14	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, septaplerin reductase and vasotocin genes, complete cds
3600	16204		1.13	6.0E-03	W37885.1	EST_HUMAN	zc13a11.1 Soares_papillary_tumor_NbHPA Homo sapiens cDNA clone IMAGE:322172 5'
3721	16322	28789	2.6	6.0E-03	BF510986.1	EST_HUMAN	UIH-B14-apm-c-08-o-01.1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3087754 3'
3721	16358	28828	1.53	6.0E-03	BE077356.1	EST_HUMAN	RC1-BT0608-260-00-014-a07 BT0608 Homo sapiens cDNA
3845	16444	28905	1.14	6.0E-03		NT	Mus musculus glucosamine-6-phosphate deaminase (Gnp1), mRNA
3995	16593	29068	0.83	6.0E-03	AW847284.1	EST_HUMAN	RCO-CT0204-240998-021-b10 CT0204 Homo sapiens cDNA
4030	16628		0.92	6.0E-03	BE250108.1	EST_HUMAN	600842904F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2859513 5'
4419	17004		1.1	6.0E-03	N58946.1	EST_HUMAN	yy62h10.s1 Soares_multiple_sclerosis_2NBHMS Homo sapiens cDNA clone IMAGE:278179 3'
4454	17040		1.58	6.0E-03	A1016833.1	EST_HUMAN	ov33c11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4805	17383	29833	8.21	6.0E-03	AA324242.1	EST_HUMAN	EST271716 Cerebellum II Homo sapiens cDNA 5' and similar to EST containing Alu repeat
5280	17852		0.92	6.0E-03	L34170.1	NT	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
6301	24761	31680	0.72	6.0E-03	9827521	NT	Varicella virus, complete genome
6908	19840	32478	0.73	6.0E-03	O14994	SWISSPROT	SYNAPSIN III
6939	18047	30489	0.72	6.0E-03	BE253748.1	EST_HUMAN	601112353F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3353172 5'
7642	20154	33040	0.76	6.0E-03	AF128894.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
7774	20283	33160	24.22	6.0E-03	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
7799	20342	33251	6.91	6.0E-03	AID33880.1	EST_HUMAN	aw13a04.x1 Soares_papillary_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1646670 3' similar to contains MER10.b1 MER10 repetitive element;
7915	20487	33363	2.45	6.0E-03	AW789337.1	EST_HUMAN	RCO-UM0051-210300-032-g02 UM0051 Homo sapiens cDNA
7990	20532		1.59	6.0E-03	BF038198.1	EST_HUMAN	601454915F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:3859628 5'
8473	21872	34821	8.46	6.0E-03	D10548.1	NT	Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein
9956	22451		2.15	6.0E-03	AI432881.1	EST_HUMAN	l122a02.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW:R13A_HUMAN
10087	22582	35557	0.73	6.0E-03	AJ011849.1	NT	P40429 60S RIBOSOMAL PROTEIN L13A ;
10197	22892		0.91	6.0E-03	AF084555.1	NT	Bacillus subtilis fnd gene
10303	22797	35788	0.63	6.0E-03	X68366.1	NT	Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds
10823	23155	36168	2.04	6.0E-03	AW982164.1	EST_HUMAN	M.thermoformicum complete plasmid pFV1 DNA
10890	23220		2.23	6.0E-03	11545814	NT	EST374237 MAGE resequences, MAGG Homo sapiens cDNA Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10726	23252	36269	2.16	6.0E-03	A1420786.1	EST_HUMAN	te91c12.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE ;
10726	23252	36270	2.16	6.0E-03	A1420786.1	EST_HUMAN	te91c12.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE ;
10861	23382		2.08	6.0E-03	U14556.1	NT	Mus musculus zinc-finger protein mRNA, complete cds
10862	23383	36401	2.4	6.0E-03	BE737895.1	EST_HUMAN	601572746F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839747 5'
11630	24072	37134	1.57	6.0E-03	H70296.1	EST_HUMAN	y95f01.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:213049 5' similar to SP:6PGD_PIG P14332 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING ;
11829	24195		3.52	6.0E-03	AF010496.1	NT	Rhodobacter capsulatus strain SB1003, partial genome
11956	24848		5.1	6.0E-03	AE000833.1	NT	Methanobacterium thermoautotrophicum from bases 429192 to 450296 (section 39 of 149) of the complete genome
12039	24914		3.02	6.0E-03	U30780.1	NT	Pneumocystis carinii f. sp. ratt guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
12088	24357		1.61	6.0E-03	Q62209	SWISSPROT	SYNAPTOMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN)
12402	24561		1.49	6.0E-03	BE768019.1	EST_HUMAN	601482621F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885388 5'
12418	24571		1.52	6.0E-03	AJ245480.1	NT	Brassica napus slg gene for S-locus glycoprotein, cultivar T2
12558	24942		1.6	6.0E-03	X74807.1	NT	R.norvegicus VEGP2 gene
229	12889	25375	5.16	5.0E-03	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
697	13320	25806	1.73	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
697	13320	25807	1.73	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
698	13320	25806	2.74	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
698	13320	25807	2.74	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORFB; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE-like protein, complete cds
1151	13754	26264	0.91	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH3
2706	15283	27830	2.77	5.0E-03	AB033006.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
2962	15578	28057	0.68	5.0E-03	BE268057.1	EST_HUMAN	601194796F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538799 5'
3170	15784	28256	4.54	5.0E-03	T87623.1	EST_HUMAN	yc81f03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:22395 3'
3189	15801		2.22	5.0E-03	AL161491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3202	15814	28289	1.15	5.0E-03	R71794.1	EST_HUMAN	y98g02.s1 Soares breast 2NIBHst Homo sapiens cDNA clone IMAGE:155666 3'
3316	15928		0.86	5.0E-03	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3728	16329	28795	5.04	5.0E-03	AL163295.2	NT	Homo sapiens chromosome 21 segment HS21C085
3762	16363	28831	4.88	5.0E-03	AF147448.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (penB) gene, complete cds
3822	16422	28884	0.68	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4043	16641		1.78	5.0E-03	AA286675.1	EST_HUMAN	EST121218 Uterus tumor 1 Homo sapiens cDNA 5' end
4204	16783	29239	0.57	5.0E-03	AJ002125.1	NT	Natrix domestica Zfx type gene
4392	16978	29425	0.88	5.0E-03	H78355.1	EST_HUMAN	yJ78g10.17 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:240068 5'
4394	16422	28884	0.71	5.0E-03	U38914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4670	17252	29704	0.68	5.0E-03	U46891.1	NT	Human putative chromatin structure regulator (SUPT6H) mRNA, complete cds
4714	17285	29739	0.8	5.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
4828	17406	29860	1.72	5.0E-03	AJ752387.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
5067	17840	30083	1.02	5.0E-03	P15285	SWISSPROT	SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)
5391	17949	30362	0.95	5.0E-03	AF171666.1	NT	Bos taurus acidic alpha-glucosidase gene, exons 2 through 20 and complete cds
5964	18586	31320	7.68	5.0E-03	P35500	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)
							PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME)
6195	18805	31574	2.33	5.0E-03	Q00507	SWISSPROT	Chlamydomonas reinhardtii AR39, section 52 of 94 of the complete genome
6230	18839		0.91	5.0E-03	AE002234.2	NT	600944584T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2890871 3'
6708	18302		10.88	5.0E-03	BE300091.1	EST_HUMAN	Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds
6932	18040	30483	6.39	5.0E-03	AB025024.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
7108	19448		0.85	5.0E-03	AB039267.1	NT	RC3-CT0255-031089-011-407 CT0255 Homo sapiens cDNA
7595	20109		1.16	5.0E-03	AW854327.1	EST_HUMAN	Homo sapiens MASL1 mRNA, complete cds
7744	20252	33146	7.43	5.0E-03	AB016816.1	NT	RC6-CT0281-081199-011-A05 CT0281 Homo sapiens cDNA
8162	20703	33618	1	5.0E-03	AW855907.1	EST_HUMAN	RC6-CT0281-081199-011-A05 CT0281 Homo sapiens cDNA
8162	20703	33619	1	5.0E-03	AW855907.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
8181	20722	33636	2.26	5.0E-03	P49882	SWISSPROT	Mouse complement receptor (CR2) mRNA, 3' end
8548	21087		6.36	5.0E-03	M61132.1	NT	Escherichia coli genomic DNA. (19.1 - 19.4 min)
8742	21281	34204	1.47	5.0E-03	D96723.1	NT	Rabbit uteroglobin (UGL) gene, exon 1
8870	21408	34333	0.69	5.0E-03	M25090.1	NT	SOF1 PROTEIN
9503	22003	34860	0.45	5.0E-03	P33750	SWISSPROT	Plasmodium berghei 58 kDa phosphoprotein mRNA, partial cds
9753	22251	35234	0.82	5.0E-03	L21710.1	NT	RCO-ST0379-210100-032-c02 ST0379 Homo sapiens cDNA
9881	22378	35354	0.77	5.0E-03	AW821898.1	EST_HUMAN	nJ46h10.s1 NCJ_CGAP_Pf8 Homo sapiens cDNA clone IMAGE:995587
10082	22557	35552	0.49	5.0E-03	AA533143.1	EST_HUMAN	

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10236	22731	35722	0.92	5.0E-03	7662567	NT	Homo sapiens PRO0471 protein (PRO0471), mRNA
10599	23133		10.33	5.0E-03	T19586.1	EST_HUMAN	694F Heart Homo sapiens cDNA clone 694
10631	23163	36175	2.28	5.0E-03	D26273.1	NT	Unknown nitrogen-fixing bacteria nifD gene encoding alpha subunit of dinitrogenase (MoFe protein)
10819	23340	36354	2.94	5.0E-03	AW170334.1	EST_HUMAN	xs5905.x1 Soares_NH-CeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1 L2 L1 repetitive element
10819	23340	36355	2.94	5.0E-03	AW170334.1	EST_HUMAN	xs5905.x1 Soares_NH-CeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2688040 3' similar to contains L1 L2 L1 repetitive element
10920	23439	36480	2.02	5.0E-03	T49153.1	EST_HUMAN	y09904.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:70686 5'
11212	23715		3.91	5.0E-03	BE048055.1	EST_HUMAN	tz46c04.y1 NCL_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291822 5'
11972	25054		8.12	5.0E-03	AF047874.1	NT	Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
12111	24372		21.73	5.0E-03	AF067253.1	NT	Brugia malayi Y chromosome marker
12217	24440		1.81	5.0E-03	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
12250	24461		1.78	5.0E-03	AA455597.1	EST_HUMAN	z775g03.s1 Soares ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:809548 3' similar to SW:DXA2_MOUSE P14685 PROBABLE DIPHENOL OXIDASE A2 COMPONENT
12283	24856		5.46	5.0E-03	BF572332.1	EST_HUMAN	60207774F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4252002 5'
12473	24598	30883	2.21	5.0E-03	AW440109.1	EST_HUMAN	UI-H-BI3-akf4-08-0-UI.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734215 3'
12498	24932		1.42	5.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
253	12913	25387	2.58	4.0E-03	AW500196.1	EST_HUMAN	UIHF-BND-akc-h-04-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078831 5'
343	12985	25480	1.77	4.0E-03	R46482.1	EST_HUMAN	y951e04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35988 3'
468	13101	25584	0.69	4.0E-03	P54675	SWISSPROT	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)
629	13256	25730	3.12	4.0E-03	AA839339.1	EST_HUMAN	on75g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562566 3'
910	13523	26043	1.75	4.0E-03	R46482.1	EST_HUMAN	y951e04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35988 3'
944	13557		3.19	4.0E-03	AW746101.1	EST_HUMAN	RC3-BT0333-110100-012401 BT0333 Homo sapiens cDNA
1190	13791	26302	25.91	4.0E-03	AA096777.1	EST_HUMAN	z81a08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5'
1211	13811	26325	1.71	4.0E-03	AW794740.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
1346	13941	26463	1.4	4.0E-03	AA284374.1	EST_HUMAN	zs59e01.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701736 5'
1630	14222		1.06	4.0E-03	AV706305.1	EST_HUMAN	AV706305 ADC Homo sapiens cDNA clone ADCAKB06 5'
1779	14369	26913	2.74	4.0E-03	U33472.1	NT	Rattus norvegicus type 1 astrocyte and olfactory-limbic associated protein AT1-46 mRNA, complete cds
2082	14842	27217	14.12	4.0E-03	AA099777.1	EST_HUMAN	z81a08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5'
2289	14863		1.62	4.0E-03	BE410556.1	EST_HUMAN	601304161F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638510 5'
2317	14889	27464	2.63	4.0E-03	AW784740.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2608	15170	27737	1.6	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2608	15170	27738	1.6	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
2715	15272	27838	3.14	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2715	15272	27839	3.14	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2721	15277	27842	1.25	4.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3262	15874	28355	1.07	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151289-003-h08 HT0340 Homo sapiens cDNA
3262	15874	28356	1.07	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151289-003-h08 HT0340 Homo sapiens cDNA
3583	16187	28670	0.85	4.0E-03	AW188426.1	EST_HUMAN	x98704.x1 NCL_CGAP_Col18 Homo sapiens cDNA clone IMAGE:2665279.3
3583	16187	28670	0.85	4.0E-03	AW188426.1	EST_HUMAN	x98704.x1 NCL_CGAP_Col18 Homo sapiens cDNA clone IMAGE:2665279.3
3685	16286	28755	0.63	4.0E-03	Q13606	SWISSPROT	OLFACTORY RECEPTOR 51 (OLFATORY RECEPTOR-LIKE PROTEIN OLF1)
3696	16287	28767	0.63	4.0E-03	AV646253.1	EST_HUMAN	AV646253 GLC Homo sapiens cDNA clone GLCADO2.3
4067	16663		1.93	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
4323	16908	28350	1.88	4.0E-03	A1768727.1	EST_HUMAN	w87a06.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400274.3
5307	17899	30291	2.1	4.0E-03	AW103719.1	EST_HUMAN	xa83d03.x1 NCL_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2814469.3 similar to contains L1 L1
5354	17914	30329	1.17	4.0E-03	AA699995.1	EST_HUMAN	L1 repetitive element :
5433	17989	30395	1.19	4.0E-03	AL163284.2	NT	269601.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:436009.3
5480	18114	30523	1.36	4.0E-03	AF005859.1	NT	Homo sapiens chromosome 21 segment HS21C084
5596	18226	30673	21.16	4.0E-03	AF169825.1	NT	Drosophila melanogaster anon2D7 (anon2D7) mRNA, complete cds
5963	18585	31319	3.31	4.0E-03	P04196	SWISSPROT	Rattus norvegicus beta-catenin binding protein mRNA, complete cds
5965	18587	31321	1.56	4.0E-03	P21849	SWISSPROT	(HPRG)
6042	18661	31400	0.97	4.0E-03	AL133871.1	EST_HUMAN	MAJOR SURFACE-LABELLED TROPHOBLAST ANTIGEN PRECURSOR
6235	18844		3.41	4.0E-03	U22180.1	NT	DKFZp7811014.1_1 781 (synonym: hamy2) Homo sapiens cDNA clone DKFZp7811014.5
6381	18985	31765	0.98	4.0E-03	AW590572.1	EST_HUMAN	Rattus norvegicus opsin gene, complete cds
6451	19052	31837	1.95	4.0E-03	BE548453.1	EST_HUMAN	hg48c07.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2948652.3
6775	19367	32179	1.04	4.0E-03	AA813222.1	EST_HUMAN	601076015F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461954.5
6872	19606	32440	1.51	4.0E-03	U76408.1	NT	aj3211.s1 Soares_testis_NHT Homo sapiens cDNA clone 1392045.3
7130	19470	32288	1.13	4.0E-03	AL163278.2	NT	Lycopersicon esculentum knotted 3 protein (TKn3) mRNA, complete cds
7130	19470	32288	1.13	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7249	19778	32633	5.45	4.0E-03	Q02817	SWISSPROT	Homo sapiens chromosome 21 segment HS21C078
							MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7459	19982	32847	1.14	4.0E-03	AI881483.1	EST_HUMAN	bx37g12.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2271814 3'
7461	19984	32849	0.95	4.0E-03	BE670170.1	EST_HUMAN	7a31b02.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284043 3'
7893	20425	33334	0.63	4.0E-03	Q9TT92	SWISSPROT	ADAM-TS 5 (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5) (ADAMTS-5) (ADAM-TS5) (AGGRECANASE-2) (ADMP-2) (ADAM-TS 11)
7992	20534	33438	4.22	4.0E-03	AF111944.1	NT	Dicystatellum discoidum AX4 development protein DGT122 (DGT122) gene, partial cds
8145	20686	33598	1.94	4.0E-03	7662067	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
8648	21187	34105	6.89	4.0E-03	AI553983.1	EST_HUMAN	te49b11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090013 3' similar to contains Alu repetitive element
8821	21360		4.46	4.0E-03	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8830	21369	34293	3.12	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
9840	22338	35319	0.78	4.0E-03	H30864.1	EST_HUMAN	yp42g12.r1 Soares retina N2b5HR Homo sapiens cDNA clone IMAGE:190150 5'
10278	22773	35762	0.7	4.0E-03	AL161555.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 55
11009	23523	36557	6.06	4.0E-03	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
11393	23845	36909	1.69	4.0E-03	AI208703.1	EST_HUMAN	qg56c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839176 3'
11393	23845	36910	1.69	4.0E-03	AI208703.1	EST_HUMAN	qg56c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839176 3'
11907	24050	37116	1.62	4.0E-03	AE002102.1	NT	Ureaplasma urealyticum section 3 of 59 of the complete genome
11938	25071		10.45	4.0E-03	BE815173.1	EST_HUMAN	PM4-BN0138-180600-002-b08 BN0138 Homo sapiens cDNA
11962	24284		1.62	4.0E-03	BE298290.1	EST_HUMAN	601118164F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5'
12047	24331		2.71	4.0E-03	AW504273.1	EST_HUMAN	UI-HF-BN0-alp-g-04-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080622 5'
12294	24493		3.86	4.0E-03	BF224125.1	EST_HUMAN	7q74c09.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3' similar to contains Alu repetitive element; contains element MER31 repetitive element ;
12341	24975		2.24	4.0E-03	AW614596.1	EST_HUMAN	hh02c07.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953932 3' similar to contains element LTR5 repetitive element ;
12352	24532		3.01	4.0E-03	AW819141.1	EST_HUMAN	RC3-ST0281-240400-015-f03 ST0281 Homo sapiens cDNA
394	13040	25531	1.73	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
912	13525	26044	5.57	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1701	14294	26829	2.85	3.0E-03	AA468110.1	EST_HUMAN	nc73c05.s1 NCI CGAP_P12 Homo sapiens cDNA clone IMAGE:782984 similar to contains Alu repetitive element;
2298	14871		1.76	3.0E-03	AF055066.1	NT	Homo sapiens MHC class 1 region
2333	14904		4.14	3.0E-03	Z32521.1	NT	S.cereale (cv. Halo) mRNA for triosephosphate isomerase
2334	14905	27475	1.03	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
2334	14905	27476	1.03	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
2448	15015	27587	1.13	3.0E-03	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3022	15638		0.66	3.0E-03	Y09006.1	NT	Arabidopsis thaliana rpoMt gene
3119	15733	28203	3.25	3.0E-03	BE379286.1	EST_HUMAN	601237982F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609933 5'
3186	15788	28270	3.21	3.0E-03	AW602887.1	EST_HUMAN	IL2-JM0076-240300-056-D03 UM0076 Homo sapiens cDNA
3464	16071	28544	2.13	3.0E-03	U34606.1	NT	Mus musculus alpha-1(XVII) collagen (COL18A1) gene, exon 1 and 2
3473	16079		7.31	3.0E-03	Y12500.1	NT	C.elegans samdc gene
4049	16646	28114	7.57	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4048	16646	28115	7.57	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4108	16703	28156	1.75	3.0E-03	AT92278.1	EST_HUMAN	ah04109.y6 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1155689 5'
4485	17070	28520	6.2	3.0E-03	AJ011432.1	NT	Rattus norvegicus gdnf gene
4560	17143		0.71	3.0E-03	BE348739.1	EST_HUMAN	h68g08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3151834 3'
4616	17188	28647	5.73	3.0E-03	AE536141.1	EST_HUMAN	xu8.P10.H3 conorm Homo sapiens cDNA 3'
4960	17535	28977	2.45	3.0E-03	AT32754.1	EST_HUMAN	ab18a08.x5 Strabegene lung (#837210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element
4979	17553	28986	6.1	3.0E-03	BE787845.1	EST_HUMAN	601482719F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:3885483 5'
5069	17642	30084	1.01	3.0E-03	AJ007044.1	NT	Oryctolagus Cuniculus sod gene
5069	17642	30085	1.01	3.0E-03	AJ007044.1	NT	Oryctolagus Cuniculus sod gene
5470	18104	30423	3.56	3.0E-03	8922499	NT	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
5744	18370	31078	1.18	3.0E-03	AJ249681.1	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)
5808	18434	31165	13.97	3.0E-03	U35323.1	NT	Mus musculus H2-M alpha chain (H2-Ma) gene, H2-M beta 2 chain (H2-Mb2) gene, H2-M beta 1 chain (H2-Mb1) gene, low molecular weight protein 2 Lmp2 (Lmp2) gene, complete cds
6670	19268	32070	10.41	3.0E-03	AA456701.1	EST_HUMAN	aal13f10.r1 Soares_NHMPu_31 Homo sapiens cDNA clone IMAGE:813163 5'
7256	19784	32640	1.45	3.0E-03	AJ011419.1	NT	Kluyveromyces fragilis pop3 gene for purine-cytosine permease
7531	20051	32824	3.37	3.0E-03	AB021736.1	NT	Oryza sativa gene for bZIP protein, complete cds
7879	20421	33329	0.91	3.0E-03	BF333058.1	EST_HUMAN	RC0-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
7879	20421	33330	0.91	3.0E-03	BF333058.1	EST_HUMAN	RC0-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
8097	20638	33548	4.71	3.0E-03	N92580.1	EST_HUMAN	zb27604.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:304783 3'
8257	20798		0.55	3.0E-03	M63498.1	NT	S. cerevisiae UGA35 gene, complete cds
8397	20937	33860	1.11	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
8419	20959	33877	1.31	3.0E-03	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C088
8522	21061		1.37	3.0E-03	Q9QM81	SWISSPROT	NONSTRUCTURAL PROTEIN V
8922	21460		12.62	3.0E-03	AW613774.1	EST_HUMAN	hh80f10.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2868131 3' similar to contains L1.H1 L1 repetitive element
8975	21513	34436	4.44	3.0E-03	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8999	21536	34466	6.98	3.0E-03	AI016731.1	EST_HUMAN	ov03121.x1 NCI CGAP_K1d3 Homo sapiens cDNA clone IMAGE:1636247 3' similar to gb:X57138_maf
9008	21545	34474	0.92	3.0E-03	BF338078.1	EST_HUMAN	HISTONE H2B.2 (HUMAN);
9330	21844		1	3.0E-03	D90801.1	NT	602035980F1 NCI CGAP_Binf64 Homo sapiens cDNA clone IMAGE:4183938 5'
9368	20307	33210	0.66	3.0E-03	BE154670.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 3/27, 271600-402289
9554	22054		0.67	3.0E-03	P03355	SWISSPROT	PM3-HT0344-071289-003-007 HT0344 Homo sapiens cDNA
9823	22123		5.92	3.0E-03	P08672	SWISSPROT	POL POLYPOLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
							CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
							RETROVIRUS-RELATED POL POLYPOLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE;
							ENDONUCLEASE]
9809	22307	35291	1.58	3.0E-03	P11369	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
9907	22404	35379	1.3	3.0E-03	P51989	SWISSPROT	Homo sapiens chromosome 21 segment HS21C103
10046	22541	35538	3.96	3.0E-03	AL163303.2	NT	Homo sapiens ATP/GTP-binding protein (HEAB), mRNA
10728	23254		4.26	3.0E-03	5803028	NT	Pneumocystis carinii kexin-like serine endoprotease mRNA, partial cds
11257	23787	36843	2.21	3.0E-03	AF009222.1	NT	Homo sapiens golgin-like protein (GLP) gene, complete cds
11321	23019	36028	1.99	3.0E-03	AF266285.1	NT	Homo sapiens tritricotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11334	23808	36867	3.96	3.0E-03	AF094481.1	NT	Homo sapiens tritricotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11354	23808	36868	3.96	3.0E-03	AF094481.1	NT	
11707	24809		2.32	3.0E-03	AI525056.1	EST_HUMAN	promrna-5.E07.1 b1 tumor Homo sapiens cDNA 5'
							alpha7b10.s1 Scarses, total, fetus, N12HF8_9w Homo sapiens cDNA clone IMAGE:1622779 3' similar to
11743	24142	36763	1.31	3.0E-03	AA993154.1	EST_HUMAN	contains L1.13 MER26 repetitive element;
11804	25007		1.81	3.0E-03	AB009668.1	NT	Homo sapiens gene for CMP-N-acetylneuraminic acid hydroxylase, partial cds
11988	24298	30984	2.67	3.0E-03	AJ296282.1	NT	Rattus norvegicus mRNA for connexin36 (cx36 gene)
541	13172	25651	0.8	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
541	13172	25652	0.8	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
818	15426		11.05	2.0E-03	T70874.1	EST_HUMAN	yd15h03.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:108341 5'
1407	14000	26529	2.25	2.0E-03	M20783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1410	14003	26531	1.35	2.0E-03	AA661605.1	EST_HUMAN	nu8601.s1 NCI CGAP_AVI1 Homo sapiens cDNA clone IMAGE:1217593
1418	14011	26540	20.96	2.0E-03	AF284446.1	NT	Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds
							PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN
1536	14128	26664	1.04	2.0E-03	P48509	SWISSPROT	SFA-1) (CD151 ANTIGEN)
							Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome
1563	14155	26686	2.05	2.0E-03	4557836	NT	type VI) (PLOD) mRNA
1563	14155	26687	2.05	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome
1635	14227		5.58	2.0E-03	P28400	SWISSPROT	type VI) (PLOD) mRNA
							COLLAGEN ALPHA 5(V) CHAIN PRECURSOR

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1807	14397	26942	1.01	2.0E-03	AA450138.1	EST_HUMAN	z42a10.r1 Soares, total, fetus, Nb2HF8, 9w Homo sapiens cDNA clone IMAGE:789114 5'
1922	14507		0.89	2.0E-03	BE144908.1	EST_HUMAN	CM2-HT0183-061099-018-d03 HT0183 Homo sapiens cDNA
2038	14820	27188	1.25	2.0E-03	AF302891.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2291	14895	27440	0.97	2.0E-03	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2815	15177		4.13	2.0E-03	AW137782.1	EST_HUMAN	UI-H-B11-edi-g-10-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3463	16070	28543	4.95	2.0E-03	AA450138.1	EST_HUMAN	z42a10.r1 Soares, total, fetus, Nb2HF8, 9w Homo sapiens cDNA clone IMAGE:789114 5'
3470	16076	28549	0.78	2.0E-03	BF568955.1	EST_HUMAN	802183960T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3729	16330	28796	5.87	2.0E-03	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, P2P2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
4024	16822	29094	0.89	2.0E-03	AB040802.1	NT	Rattus norvegicus mRNA for SREB1, complete cds
4191	16780	29228	2.48	2.0E-03	PC3374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
4302	16888		12.85	2.0E-03	U88491.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds
4502	17086		1.09	2.0E-03	L35079.1	NT	Porcine rotavirus major outer capsid protein (VP7) mRNA, complete cds
4518	17102		1.34	2.0E-03	AW287380.1	EST_HUMAN	UI-H-BW0-air-g-03-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2730413 3'
4523	17107	29553	0.98	2.0E-03	AI064746.1	EST_HUMAN	HA0507 Human fetal liver cDNA library Homo sapiens cDNA
4644	17226	29680	1.82	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4644	17226	29681	1.82	2.0E-03	L42512.1	NT	Drosophila melanogaster shortighted class 2 (shs) mRNA, complete cds
4821	17398		1.82	2.0E-03	R87773.1	EST_HUMAN	yo45e02.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:180890 3'
4848	17428	29878	5.2	2.0E-03	AA1909466.1	EST_HUMAN	d14f05.s1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1523457 3'
5187	17736	30163	0.81	2.0E-03	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5426	17985		0.9	2.0E-03	AF205087.1	NT	Desulfotribio desulfuricans cytochrome c3 precursor (cypcA) gene, complete cds
5678	18305	30787	1.16	2.0E-03	BF241410.1	EST_HUMAN	801876385F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104692 5'
5810	24749	31156	2.28	2.0E-03	AB014593.1	NT	Homo sapiens mRNA for KIAA0693 protein, partial cds
5887	18510	31236	2.11	2.0E-03	U63711.1	NT	Xenopus laevis xellin mRNA, complete cds
6258	18987	31636	4.06	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6258	18987	31637	4.06	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6486	18087	31869	2.38	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-XI)
6486	18087	31870	2.38	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-XI)
6488	19088	31872	7	2.0E-03	BF308187.1	EST_HUMAN	801887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5'
8521	19121	31912	2.17	2.0E-03	Q9UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
8546	19144	31940	1.46	2.0E-03	X94451.1	NT	L. esculentum mRNA for Isyl-IRNA synthetase (LysRS)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6715	19309		2.03	2.0E-03	AI991089.1	EST_HUMAN	wu36h09.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522177 3' similar to SW:RL29 HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ;contains element MSR1 repetitive element ;
7038	18058	30480	0.89	2.0E-03	AB038502.1	NT	Caenorhabditis elegans mRNA for galectin LEC-11, complete cds
7104	19874	32513	1.54	2.0E-03	5031864	NT	Homo sapiens lipoma HMGIC fusion partner (LHFP) mRNA
7104	19874	32514	1.54	2.0E-03	5031864	NT	Homo sapiens lipoma HMGIC fusion partner (LHFP) mRNA
7141	19521	32343	3.59	2.0E-03	BE067986.1	EST_HUMAN	CM4-BT0366-081299-054-d01 BT0366 Homo sapiens cDNA
7198	19729	32580	0.7	2.0E-03	AI298883.1	EST_HUMAN	qm98d11.x1 NCLCGAP_Lu5 Homo sapiens cDNA clone IMAGE:1896885 3'
7335	19882	32726	0.87	2.0E-03	T86569.1	EST_HUMAN	yd77g10.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:114306 5'
7613	20126	33003	1.49	2.0E-03	P07354	SWISSPROT	PROTEOLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
7995	20537	33440	2.47	2.0E-03	AW592004.1	EST_HUMAN	h37606.x1 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:2934035 3' similar to TR:Q80976 Q80976 JERKY. ;
8159	20700	33614	5.96	2.0E-03	N20287.1	EST_HUMAN	yx42g06.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1 b2 L1 repetitive element ;
8159	20700	33615	5.96	2.0E-03	N20287.1	EST_HUMAN	yx42g06.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1 b2 L1 repetitive element ;
8208	20749	33682	0.52	2.0E-03	Q92350	SWISSPROT	HYPOTHETICAL 32.8 KD PROTEIN C8G9.05 IN CHROMOSOME 1
8228	20789	33688	0.94	2.0E-03	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
8282	20823	33743	0.82	2.0E-03	6005955	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8282	20823	33744	0.82	2.0E-03	6005955	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8307	20848	33771	0.8	2.0E-03	AU136879.1	EST_HUMAN	AU136879 PLACE1 Homo sapiens cDNA clone PLACE1004839 5'
8358	20898		2.04	2.0E-03	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
9123	18508	31233	0.69	2.0E-03	AW796111.1	EST_HUMAN	MR2-UMC025-300300-102-f02 UM0025 Homo sapiens cDNA
9123	18508	31234	0.69	2.0E-03	AW796111.1	EST_HUMAN	MR2-UMC025-300300-102-f02 UM0025 Homo sapiens cDNA
9184	21699	34643	0.85	2.0E-03	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9445	21971	34920	0.99	2.0E-03	H50832.1	EST_HUMAN	yp86a09.s1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:194296 3'
9445	21971	34921	0.99	2.0E-03	H50832.1	EST_HUMAN	yp86a09.s1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:194296 3'
9477	21876	34823	2.57	2.0E-03	P24821	SWISSPROT	TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEI) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C)
9585	22085	35049	1.03	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9585	22085	35050	1.03	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9639	22139	35105	0.54	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
9639	22139	35106	0.54	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
9629	22327	35308	0.98	2.0E-03	AV884269.1	EST_HUMAN	QV3-OT0084-060400-144-e01 OT0084 Homo sapiens cDNA
9955	22450		4.55	2.0E-03	AA251376.1	EST_HUMAN	zs10a06.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684754 3'
10894	23415		3.24	2.0E-03	MB5524.1	NT	Human dystrophin gene
11361	20126	33003	2.13	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
11417	23888		2.25	2.0E-03	BF330809.1	EST_HUMAN	RC3-BT0333-310800-115-g04 BT0333 Homo sapiens cDNA
11424	23875	38939	13.97	2.0E-03	Z11740.1	NT	H sapiens variable number tandem repeat (VNTR) locus DNA
11687	24103		3.17	2.0E-03	AB25745.1	EST_HUMAN	y65n03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283989 3' similar to SW:VATG_MANSE
11705	24118	37151	4.77	2.0E-03	AF157516.2	NT	Q25532 VACUOLAR ATP SYNTHASE SUBUNIT G ;
11730	24135	37155	1.94	2.0E-03	AI084325.1	EST_HUMAN	Homo sapiens SEL1L (SEL1L) gene, partial cds
11754	18032		8.96	2.0E-03	AJ245187.1	NT	oy43g06.s1 Scarses_papillary_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1688534 3' similar to
11987	25050		2.34	2.0E-03	AV697866.1	EST_HUMAN	TR:P97535 P97535 PS-PLA1 PRECURSOR ;
12062	24345	30984	1.49	2.0E-03	Y00508.1	NT	Camelus dromedarius crip19 gene for immunoglobulin heavy chain variable region
							AV697866 GKC Homo sapiens cDNA clone GKCGXD05 5'
							H. sapiens M1 gene for muscarinic acetylcholine receptor
12372	24542		2.06	2.0E-03	AF129758.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
12551	24848		5.07	2.0E-03	AV697866.1	EST_HUMAN	AV697866 GKC Homo sapiens cDNA clone GKCGXD05 5'
484	13098	25589	1.33	1.0E-03	H08471.1	EST_HUMAN	y08c08.r1 Scarses_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232334 5'
862	13477	25692	1.47	1.0E-03	AI720263.1	EST_HUMAN	as70b08.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
							Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE ;
862	13477	25693	1.47	1.0E-03	AI720263.1	EST_HUMAN	as70b08.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
1134	13737	26246	2.21	1.0E-03	AB55788.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE ;
1154	13757	26287	1.31	1.0E-03	AB54572.1	EST_HUMAN	wa86a08.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422258 3'
							wa83e10.x1 NCL_CGAP_Mal15 Homo sapiens cDNA clone IMAGE:2551242 3'
1208	13808	26321	1.67	1.0E-03	AB2616.1	EST_HUMAN	wd86a01.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338440 3' similar to contains Alu repetitive element;
2074	14654	27227	4.05	1.0E-03	P47808	SWISSPROT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMMWI)
2189	14775	27348	9.99	1.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3008	15624	28102	1.45	1.0E-03	AB033117.1	NT	Homo sapiens mRNA for KIAA1281 protein, partial cds
3225	15837	28315	1.81	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3225	15837	28316	1.81	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED
3341	15951	28427	0.79	1.0E-03	P08547	SWISSPROT	CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)
3586	16200	28683	0.65	1.0E-03	U68061.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3596	16200	28684	0.65	1.0E-03	U68061.1	NT	Human MUC2 gene, promoter region
3727	16328		1.31	1.0E-03	AB044400.1	NT	Human MUC2 gene, promoter region
3997	16595	29087	0.75	1.0E-03	AW170552.1	EST_HUMAN	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15
4008	16606	29080	0.81	1.0E-03	Z49649.1	NT	contains TAR111 TART repetitive element;
4528	17112	29556	4.29	1.0E-03	BE939162.1	EST_HUMAN	S. cerevisiae chromosome X reading frame ORF YJR149w
4574	17157	29601	5.77	1.0E-03	BE246536.1	EST_HUMAN	RC1-TN0128-160800-021-g01 TN0128 Homo sapiens cDNA
4770	17351	29803	0.83	1.0E-03	U29449.1	NT	TCBAP-1D4908 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo
4950	17525	29866	2.83	1.0E-03	A1073485.1	EST_HUMAN	sapiens cDNA clone TCBAP4909
4950	17525	29867	2.83	1.0E-03	A1073485.1	EST_HUMAN	Caenorhabditis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes
4951	17528		5.92	1.0E-03	BE164087.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262.3'
5236	17800	30219	11.45	1.0E-03	O46409	SWISSPROT	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262.3'
5511	18144	30556	2.02	1.0E-03	AA280951.1	EST_HUMAN	PMO-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA
5598	18228	30676	2.74	1.0E-03	AJ006345.1	NT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
5647	18275	30749	1.7	1.0E-03	K03332.1	NT	zs44f01.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700345.5'
5647	18275	30750	1.7	1.0E-03	K03332.1	NT	Homo sapiens KVLQ11 gene
5761	18387	31101	0.92	1.0E-03	BE796491.1	EST_HUMAN	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5766	18392	31105	1.72	1.0E-03	Q02388	SWISSPROT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
6171	18783		2.62	1.0E-03	X07689.1	NT	601589841F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943954.5'
6209	18819	31590	1.1	1.0E-03	BE963939.2	EST_HUMAN	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
6339	18945		8.29	1.0E-03	11526176	NT	Mouse nucleolin gene
6476	19077	31860	1.21	1.0E-03	T87761.1	EST_HUMAN	601657519R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875693.3'
6541	19140		1.4	1.0E-03	AW902585.1	EST_HUMAN	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6852	19441	32256	1.31	1.0E-03	L77570.1	NT	yd83a11.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:115772.5'
7206	19737	32590	2.48	1.0E-03	D16826.1	NT	QV3-NN1024-260400-171-g05 NN1024 Homo sapiens cDNA
7498	20021		1.72	1.0E-03	AJ28042.1	NT	Homo sapiens DGeorge syndrome critical region, centromeric end
							Human gene for fourth somatostatin receptor subtype
							Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal
7635	20147	33030	1.7	1.0E-03	U52111.2	NT	protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRT),
							CDM protein (CDM), adrenoleukodystrophy protein >

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7694	20203	33090	3.21	1.0E-03	M63376.1	NT	Human TRPM-2 protein gene, exons 1,2 and 3
7734	20242	33133	1.13	1.0E-03	BE80044.1	EST_HUMAN	801491081F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3893276 5'
7830	20372	33279	0.57	1.0E-03	AF274581.1	NT	Homo sapiens prolactin-releasing peptide receptor gene, 5' flanking region
7891	20493	33342	5.79	1.0E-03	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
8086	20627	33541	1.29	1.0E-03	AA122270.1	EST_HUMAN	zh87c09.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:490768 3' similar to contains L1.1 L1 repetitive element;
8186	20727	33639	2.03	1.0E-03	AF153980.1	NT	Homo sapiens exostoses-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
8369	20909	33828	0.81	1.0E-03	U29397.1	NT	Rattus norvegicus plasma membrane Ca2+ ATPase isoform 3 (PMCA3) gene, 5' flanking region
8530	21069	33988	0.52	1.0E-03	AA001613.1	EST_HUMAN	zh82e06.s1 Soares_fetal_liver脾脾_INFLS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
8530	21069	33989	0.52	1.0E-03	AA001613.1	EST_HUMAN	zh82e06.s1 Soares_fetal_liver脾脾_INFLS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
8873	21412		1.29	1.0E-03	Y11204.1	NT	V. carteri gene encoding volvoxopsin
8900	21439	34361	0.59	1.0E-03	AW840533.1	EST_HUMAN	CM3-LT0079-170200-092-e07 LT0079 Homo sapiens cDNA
9009	21546						Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
9047	21584	34514	0.68	1.0E-03	U32111.2	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
9047	21584	34515	3.37	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
9525	22025	34982	1.96	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (aglA) gene, complete cds
9525	22025	34983	1.96	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (aglA) gene, complete cds
9734	22322	35210	0.94	1.0E-03	Q01129	SWISSPROT	BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40) (DERMATAN SULFATE
10068	22563	35558	0.57	1.0E-03	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
10073	22598		0.75	1.0E-03	AF097495.1	NT	Homo sapiens transducin beta-like 2 (TBL2) gene, complete cds
10218	22713	35705	1.25	1.0E-03	A024350.1	EST_HUMAN	ov75f08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643175 3' similar to contains MER39.b1 MER39 MER39 repetitive element;
10545	23082	36095	1.71	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181099-011-e09 CT0279 Homo sapiens cDNA
10545	23082	36096	1.71	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181099-011-e09 CT0279 Homo sapiens cDNA
10629	23161	36173	3.2	1.0E-03	BE170856.1	EST_HUMAN	QV3-HT0543-220300-130-e03 HT0543 Homo sapiens cDNA
							tt73e12.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246446 3' similar to TR:Q28195 Q28195 PVA1 GENE;
10703	23232		3.19	1.0E-03	A1563847.1	EST_HUMAN	AV759848 MDS Homo sapiens cDNA clone MDSDDF11 5'
11036	23550		3.78	1.0E-03	AV759848.1	EST_HUMAN	801433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
11682	24098	37149	4.46	1.0E-03	BE5894488.1	EST_HUMAN	Rattus norvegicus transformation related protein 63 (Trp63), mRNA
12149	24392	30974	1.27	1.0E-03		NT	

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12175	25030		5.99	1.0E-03	AI347355.1	EST_HUMAN	tc05h11.x1 NCI_CGAP_C016 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains Alu repetitive element;
12292	25052	30510	5.72	1.0E-03	BE780572.1	EST_HUMAN	601468878F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872035 5'
5862	18484		1.63	9.0E-04	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
6612	19209	32017	1.06	9.0E-04	P02381	SWISSPROT	MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1
9561	22061		1.56	9.0E-04	AB037203.1	NT	Glycyrhiza glabra GgBAS1 mRNA for beta-amylin synthase, complete cds
1535	14127		1.05	8.0E-04	X98469.1	NT	X laevis mRNA for C4SR protein
4259	16845		5.17	8.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4880	17455	29908	2.55	8.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
11024	23538		2.15	8.0E-04	AA77084.1	EST_HUMAN	224c10.s1 Soares fetal heart NBH19W Homo sapiens cDNA clone IMAGE:377874 3'
11175	23682		2.5	8.0E-04	AI571099.1	EST_HUMAN	In85a08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2176310 3'
12500	24626	30892	1.65	8.0E-04	AW579954.1	EST_HUMAN	PM2-HT0353-130100-002-f10 HT0353 Homo sapiens cDNA
1867	14453	27012	0.99	7.0E-04	L41826.1	NT	Homo sapiens CYP17 gene, 5' end
2442	15009	27581	0.92	7.0E-04	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
2739	15294	27861	1.75	7.0E-04	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3319	15929	28406	1.23	7.0E-04	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
6246	18855	31626	0.75	7.0E-04	AA516212.1	EST_HUMAN	ng65g12.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:939718 similar to contains L1, b3 L1 L1 repetitive element;
6636	19232		2.63	7.0E-04	AI769331.1	EST_HUMAN	wg36f09.x1 Soares NSF_F8_gW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
7279	19807		0.79	7.0E-04	AK024445.1	NT	Homo sapiens mRNA for FLJ00035 protein, partial cds
9719	22217	35191	0.57	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
9719	22217	35192	0.57	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11440	23890		3.42	7.0E-04	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
11463	23913	36960	2.68	7.0E-04	Z40561.1	EST_HUMAN	HSC28A072 normalized infant brain cDNA Homo sapiens cDNA clone c-28a07 3'
12222	24443		11.57	7.0E-04	BE077041.1	EST_HUMAN	GM1-BT0614-110300-142-b12 BT0614 Homo sapiens cDNA
12472	24567		4.94	7.0E-04	R17336.1	EST_HUMAN	yg13c06.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:32298 5'
12505	24628		7.97	7.0E-04	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
2720	15276		0.93	6.0E-04	BF341380.1	EST_HUMAN	602013339F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4149297 5'
4033	16631	29100	1.61	6.0E-04	AI862525.1	EST_HUMAN	wy15a11.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402876 3'
4163	16754	29205	0.6	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4163	16754	29206	0.6	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4264	16850	29298	3.2	6.0E-04	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
4538	17122	29567	0.93	6.0E-04	BE173435.1	EST_HUMAN	RC2-HT0560-190200-011-009 HT0560 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4538	17122	29568	0.93	6.0E-04	BE173435.1	EST_HUMAN	RC2-HT0560-180200-011-409 HT0560 Homo sapiens cDNA
5413	17970	30379	0.9	6.0E-04	AI906667.1	EST_HUMAN	RC-BT122-180398-057 BT122 Homo sapiens cDNA
5413	17970	30380	0.9	6.0E-04	AI906667.1	EST_HUMAN	RC-BT122-180398-057 BT122 Homo sapiens cDNA
7807	20350		3.04	6.0E-04	P46408	SWISSPROT	GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER)
7958	20500		0.67	6.0E-04	H92947.1	EST_HUMAN	y94c11.s1 Soares_pinea_gland_N3HPG Homo sapiens cDNA clone IMAGE:231956 3' similar to contains LOR1 repetitive element.
9890	22387		3.74	6.0E-04	AL048507.2	EST_HUMAN	DKFZ586M2024_r1 586 (synonym: huter1) Homo sapiens cDNA clone DKFZ586M2024
9924	22420		0.77	6.0E-04	AI858286.1	EST_HUMAN	w835g02.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2426930 3'
9992	22487	35475	2.18	6.0E-04	BE005850.1	EST_HUMAN	RC2-BN0120-250400-012-h11 BN0120 Homo sapiens cDNA
10242	22737		0.64	6.0E-04	AF287478.1	NT	Lytechinus variegatus embryonic blastocoel extracellular matrix protein precursor (ECM3) mRNA, complete cds
11358	23812	36872	2.9	6.0E-04	AJ229042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
11441	23861	36856	5.11	6.0E-04	AW013847.1	EST_HUMAN	UI-H-BI0-aab-e-09-0-J1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
11495	23944		2.28	6.0E-04	Q01768	SWISSPROT	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) (NM23-M2) (P18)
11869	24928		3.55	6.0E-04	AW380519.1	EST_HUMAN	RC1-HT0289-281199-012-408 HT0289 Homo sapiens cDNA
12671	24739		1.61	6.0E-04	AI817088.1	EST_HUMAN	wj76g11.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408804 3' similar to contains element L1 repetitive element.
679	13303	25785	8.64	5.0E-04	O10341	SWISSPROT	HYPOTHETICAL_29.3 KD PROTEIN (ORF92)
1549	14141		1.68	5.0E-04	AW851844.1	EST_HUMAN	QV0-CT0225-021099-030-e07 CT0225 Homo sapiens cDNA
3460	16067	28540	1.53	5.0E-04	AA548931.1	EST_HUMAN	nk27e11.s1 NCI_CGAP_Cot11 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu repetitive element.
3778	16378	28843	1.02	5.0E-04	Q9UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
5684	18291	30770	1.98	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6740	19334	32141	6.37	5.0E-04	AA156080.1	EST_HUMAN	zo33b08.r1 Stragene colon (#837204) Homo sapiens cDNA clone IMAGE:588663 5'
7411	19936	32801	16.91	5.0E-04	M23604.1	NT	Gorilla gorilla involucrin gene medium allele, complete cds
7898	20440	33346	4.97	5.0E-04	AI188382.1	EST_HUMAN	qd13f06.x1 Soares_placenta_8tc9weeks_2Nhp8P8c9W Homo sapiens cDNA clone IMAGE:1723619 3' similar to gb:X51602_cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN)/contains Alu repetitive element.
8245	20786	33705	0.91	5.0E-04	AA814519.1	EST_HUMAN	cd96a02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1339226 3' similar to contains element MER22 repetitive element.
9201	21718	34662	1.37	5.0E-04	AA846545.1	EST_HUMAN	aj56h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1384357 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9263	21963	34840	0.6	5.0E-04	N83765.1	EST_HUMAN	KK2745F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK2745 5' similar to REPEITIVE ELEMENT
9437	21963	34912	0.65	5.0E-04	P29126	SWISSPROT	BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XYLA PRECURSOR
9527	22027	34966	4.43	5.0E-04	AW270938.1	EST_HUMAN	xs06a02.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2768858 3'
10855	23376		4.52	5.0E-04	AL048507.2	EST_HUMAN	DKFZp586M2024_r1 596 (synonym: hute1) Homo sapiens cDNA clone DKFZp586M2024
11559	18291	30770	11.05	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
11631	19936	32801	1.84	5.0E-04	M23804.1	NT	Gorilla gorilla involucrin gene medium allele, complete cds
11809	24857		3.21	5.0E-04	AA588513.1	EST_HUMAN	nf15h02.s1 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:913875
12353	24883		1.77	5.0E-04	U63834.1	NT	Human KIT protein and alternatively spliced KIT protein (KIT) gene, complete cds
415	13050		0.64	4.0E-04	BF241482.1	EST_HUMAN	601878534F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104897 5'
701	13323	-25810	1.12	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 63 of 163 of the complete genome
880	13494	26012	1.46	4.0E-04	A1720263.1	EST_HUMAN	as70b08.x1 Barslead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
880	13494	26013	1.46	4.0E-04	A1720263.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE.1
1514	14106	26642	9.82	4.0E-04	AW753356.1	EST_HUMAN	as70b08.x1 Barslead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
2130	14708	27280	1.59	4.0E-04	AL163278.2	NT	RC3-CT0254-130100-023-101 CT0254 Homo sapiens cDNA
2179	14756		1.34	4.0E-04	AL046704.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
2656	15215	27787	1.83	4.0E-04	O66615	SWISSPROT	DKFZp434D059_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D059 5'
3200	15812	28286	2.59	4.0E-04	AF281074.1	NT	SERICIN-2 (SILK GUM PROTEIN 2)
3405	16014	28493	0.58	4.0E-04	AV696624.1	EST_HUMAN	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3635	16533		0.94	4.0E-04	AL163267.2	NT	AV696624 GK Homo sapiens cDNA clone GKCFH07 5'
4415	17000	29442	3.2	4.0E-04	AA576331.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C067
4415	17000	29443	3.2	4.0E-04	AA576331.1	EST_HUMAN	nh10a10.s1 NCL_CGAP_Cot1 Homo sapiens cDNA clone IMAGE:951830 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4635	17218	29871	1.94	4.0E-04	AA086324.1	EST_HUMAN	nh10a10.s1 NCL_CGAP_Cot1 Homo sapiens cDNA clone IMAGE:951830 3' similar to gb:M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
5249	17812	30235	6.04	4.0E-04	BE560660.1	EST_HUMAN	zn61c08.s1 Stragelene muscle 937209 Homo sapiens cDNA clone IMAGE:562670 3'
7312	19840	32699	1.25	4.0E-04	P48442	SWISSPROT	601345895F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3678910 5'
7541	20061		2.42	4.0E-04	AL161566.2	NT	EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL CALCIUM-SENSING RECEPTOR)
8473	21013	33929	1.42	4.0E-04	BF240712.1	EST_HUMAN	CALCIUM-SENSING RECEPTOR
8481	21020	33935	1.85	4.0E-04	N25507.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 66
							601875685F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099700 5'
							yx39a12.r1 Soares melanocyte 2Nbl-1M Homo sapiens cDNA clone IMAGE:264142 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9008	22108	35070	2.79	4.0E-04	AI025699.1	EST_HUMAN	087h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1844341 3'
9754	22552		1.22	4.0E-04	AF022855.1	NT	Mus musculus neuropilin-2(a17) mRNA, alternatively spliced, complete cds
12188	24833		2.4	4.0E-04	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
187	12830	25318	2.71	3.0E-04	AL119428.1	EST_HUMAN	DKFZp761J221_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J221 5'
209	12870	25356	3.63	3.0E-04	P49259	SWISSPROT	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
913	13526	28045	1.72	3.0E-04	U83991.1	NT	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
1879	14465	27022	5.5	3.0E-04	AI262100.1	EST_HUMAN	q228d03.y1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028197 5'
1894	14479		1.08	3.0E-04	AI399674.1	EST_HUMAN	th23a02.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2119082 3'
3349	19568	28434	4.95	3.0E-04	P25147	SWISSPROT	INTERNALIN B PRECURSOR
4038	19634	29103	3.07	3.0E-04	P49448	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4131	18723		1.37	3.0E-04	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4167	16758		1.14	3.0E-04	BE140609.1	EST_HUMAN	RCO-H10014-3.10599-028 HT0014 Homo sapiens cDNA
4941	17516		5.05	3.0E-04	BE153778.1	EST_HUMAN	PMO-HT0339-190200-007-g12 HT0339 Homo sapiens cDNA
5162	17731	30158	0.57	3.0E-04	Q09472	SWISSPROT	E1A-ASSOCIATED PROTEIN P300
6292	18900		5.93	3.0E-04	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
6909	19568	32395	1.67	3.0E-04	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7590	20105	32981	1.04	3.0E-04	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
8202	20743	33656	6.76	3.0E-04	P22807	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
9834	22332	35313	1.46	3.0E-04	AA454055.1	EST_HUMAN	zx48d08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795471 5' similar to gb.M62762
10080	22575	35570	0.5	3.0E-04	AI92139.1	EST_HUMAN	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN);
							wt75a11.x1 Soares_thymus_NHTFth Homo sapiens cDNA clone IMAGE:2513278 3'
							ai24g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:2513278 3'
10356	22850	35844	8.78	3.0E-04	AA781201.1	EST_HUMAN	RIBOSOMAL PROTEIN L7A (HUMAN);
							nc38a04.r1 NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1.12 L1
							repetitive element;
11758	25072	30514	3.55	3.0E-04	AA228301.1	EST_HUMAN	Homo sapiens mRNA for KIAA0749 protein, partial cds
12140	24909	30713	4.29	3.0E-04	AB018292.1	NT	DKFZp547L185_r1 547 (synonym: Mbr1) Homo sapiens cDNA clone DKFZp547L185 5'
12574	24671		3.54	3.0E-04	AL134483.1	EST_HUMAN	Homo sapiens SCG10 like-protein, helix-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
187	12848	25333	1.23	2.0E-04	AF217798.1	NT	Homo sapiens SCG10 like-protein, helix-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
504	13136	25624	2.86	2.0E-04	AU146707.1	EST_HUMAN	AU146707 HEMBB1 Homo sapiens cDNA clone HEMBB1001253 3'
940	13553	26068	5.4	2.0E-04	MB6524.1	NT	Human dystrophin gene
940	13553	26070	5.4	2.0E-04	MB6524.1	NT	Human dystrophin gene
1221	13821		3.94	2.0E-04	AI266021.1	EST_HUMAN	qh98e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3 b2 MER3 repetitive element;

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1228	13827		1.95	2.0E-04	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1872	14458		1.12	2.0E-04	AF224268.1	NT	Mus musculus 5' flanking region of Pitx3 gene
2227	14802		0.9	2.0E-04	AA478980.1	EST_HUMAN	zu39b05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alu repetitive element.
2810	15172	27740	6.83	2.0E-04	U68081.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2, >
3016	15632	28109	1.13	2.0E-04	AI124529.1	EST_HUMAN	am58c09.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539760 3'
3377	15986	28464	0.76	2.0E-04	5174736	NT	Homo sapiens tubulin, beta, 4 (TUBB4) mRNA
3483	16089	28561	2.53	2.0E-04	BE082317.1	EST_HUMAN	QV2-BT0638-070500-194-b07 BT0638 Homo sapiens cDNA
3983	16581	28052	0.85	2.0E-04	AW978441.1	EST_HUMAN	EST390550 IMAGE resequences, MAGP Homo sapiens cDNA
4224	16812		6.34	2.0E-04	U01028.1	NT	Phasodolus vulgaris nitrate reductase (PvNIR2) gene, complete cds
4776	17357	29809	1.34	2.0E-04	H90265.1	EST_HUMAN	y01e11.1 Soares pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4776	17357	29810	1.34	2.0E-04	H90265.1	EST_HUMAN	y01e11.1 Soares pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232556 5'
4913	17488		1.79	2.0E-04	U98226.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
5215	17780	30109	1.44	2.0E-04	AB037997.1	NT	Danio rerio hagoromo gene, exons 1 to 6, partial cds
5733	18359	31065	1.92	2.0E-04	AV654352.1	EST_HUMAN	AV654352 GLC Homo sapiens cDNA clone GLCDUH10 3'
5745	18371	31078	1.87	2.0E-04	AI690882.1	EST_HUMAN	tp03b11.x1 NCL_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207709 3'
5924	18546	31272	0.87	2.0E-04	AA296652.1	EST_HUMAN	EST11181 Uterus Homo sapiens cDNA 5' end similar to EST containing O family repeat
6102	18718	31470	1.06	2.0E-04	4758179	NT	Homo sapiens cell cycle progression 3 protein (DNJ3) mRNA
6385	18989	31769	0.81	2.0E-04	AF140708.1	NT	Mus musculus G protein coupled receptor gene, complete cds; and unknown gene
7281	19809		2.44	2.0E-04	AU121712.1	EST_HUMAN	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000798 5'
7616	20129		13.08	2.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7626	20138	33017	1.26	2.0E-04	P54296	SWISSPROT	MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)
7897	20439	33344	2.74	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
7897	20439	33345	2.74	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8226	20767	33685	0.97	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8226	20767	33686	0.97	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8500	21039	33960	1.77	2.0E-04	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHLT) gene, exon 5

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8678	21217	34137	0.56	2.0E-04	X57331.1	NT	Human immunoglobulin C(mu) and C(delta) heavy chain genes (constant regions)
9257	21783	34736	0.47	2.0E-04	AA728700.1	EST_HUMAN	ai22a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343518 3'
9340	21854	34803	0.5	2.0E-04	P18715	SWISSPROT	GASTRULA ZINC FINGER PROTEIN XLCGF26.1
9885	22382	35357	1.4	2.0E-04	BE149303.1	EST_HUMAN	RC3-HT0254-151089-011-b05 HT0254 Homo sapiens cDNA
9830	22426	35400	2.39	2.0E-04	AA405777.1	EST_HUMAN	zu66c11.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:742864 5'
10731	23257	36273	6.22	2.0E-04	AV730373.1	EST_HUMAN	AV730373 HTF Homo sapiens cDNA clone HTFAAA01 5'
11185	23690	36737	5.43	2.0E-04	A1440282.1	EST_HUMAN	q0111.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element
11303	23796	36854	2.72	2.0E-04	AW138740.1	EST_HUMAN	UH-B1-adm-c-04-Q-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717190 3'
799	13416	25920	1.41	1.0E-04	H96846.1	EST_HUMAN	y26c09.s1 Soares_melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:262864 3' similar to contains L1.1 L1 repetitive element
1113	13717	26227	2.57	1.0E-04	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
1153	13756	26265	4.04	1.0E-04	AW013847.1	EST_HUMAN	UH-B10-sab-e-09-Q-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1153	13756	26266	4.04	1.0E-04	AW013847.1	EST_HUMAN	UH-B10-sab-e-09-Q-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1377	13970		3.95	1.0E-04	U62918.1	NT	Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds
1669	14282	26795	2.57	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1669	14262	26796	2.57	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 68 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylformylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1801	14486	27047	2.44	1.0E-04	AB048342.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TKY38
2711	15288	27835	1.09	1.0E-04	BE218833.1	EST_HUMAN	h45c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3178366 3'
2711	15288	27836	1.09	1.0E-04	BE218833.1	EST_HUMAN	h45c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3178366 3'
3323	15633	28410	1.1	1.0E-04	Q62203	SWISSPROT	SPICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
3799	16399	28864	2.7	1.0E-04	A1440282.1	EST_HUMAN	q0111.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element
4134	16726	29180	1.72	1.0E-04	M14042.1	NT	Mouse alpha 1 type-IV collagen mRNA
4156	16748	29201	1.27	1.0E-04	AV647727.1	EST_HUMAN	AV647727 GLC Homo sapiens cDNA clone GLCBB004 3'
5283	17825	30250	0.85	1.0E-04	A157156.1	EST_HUMAN	q02h04.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:2005975 3'
6021	18640	31380	1.5	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6568	19166	31962	0.97	1.0E-04	AA177111.1	EST_HUMAN	nc02e12.s1 NCI_CGAP_Pt3 Homo sapiens cDNA clone IMAGE:252

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6925	19584	32414	0.76	1.0E-04	AA564561.1	EST_HUMAN	n125a04.s1 NCL_CGAP_AA1 Homo sapiens cDNA clone IMAGE:593486 3' similar to gb.M97252 KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN); contains Alu repetitive element;
7237	19767	32623	14.09	1.0E-04	A1251980.1	EST_HUMAN	qv57d10.x1 NCL_CGAP_Ox32 Homo sapiens cDNA clone IMAGE:1985883 3'
7572	19767	32623	14.23	1.0E-04	A1251980.1	EST_HUMAN	qv57d10.x1 NCL_CGAP_Ox32 Homo sapiens cDNA clone IMAGE:1985883 3'
7937	20479	33389	1.02	1.0E-04	AA804453.1	EST_HUMAN	ab94g08.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:854854 3'
8260	21786	34738	2.34	1.0E-04	AB06220.1	EST_HUMAN	wf26e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356742 3'
9270	21786	34745	1.71	1.0E-04	O88989	SWISSPROT	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN B)
9346	21860		0.78	1.0E-04	T77153.1	EST_HUMAN	jd172c08.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:113774 5'
9864	22064	35023	2.2	1.0E-04	10863876	NT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
10081	22576		2.87	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10116	22611	35601	0.83	1.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11218	23721		2.06	1.0E-04	M28587.1	NT	Mouse alpha leukocyte interferon gene, complete cds
11503	23952	37020	1.98	1.0E-04	AB032968.1	NT	Homo sapiens mRNA for KIAA1142 protein, partial cds
11540	23988	37059	2.1	1.0E-04	AW269081.1	EST_HUMAN	xy49g12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816518 3'
11570	24017	37086	1.87	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
11570	24017	37087	1.87	1.0E-04	Q03696	SWISSPROT	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
11670	24092		1.57	1.0E-04	BE696769.1	EST_HUMAN	CMD-CT0404-130700-475-h03 CT0404 Homo sapiens cDNA
11919	24876		1.99	1.0E-04	BE676399.1	EST_HUMAN	7f28a10.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3286058 3' similar to contains L1.13 L1 repetitive element;
13347	25839		1.98	9.0E-05	AA718833.1	EST_HUMAN	ah45c11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1292468 3'
2047	14629	27188	0.92	9.0E-05	AW866218.1	EST_HUMAN	QV4-SN0023-070400-166-h04 SN0023 Homo sapiens cDNA
6117	18733	31486	1.45	9.0E-05	Q60716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
9397	21820		2.71	9.0E-05	D85606.1	NT	Homo sapiens gene for cholesterylkinin type-A receptor, complete cds
9399	21822	34771	2.79	9.0E-05	AF120982.1	NT	Homo sapiens methyl-CpG binding protein 1 (MBD1) gene, exon 15b
11017	23531		2.86	9.0E-05	AW073078.1	EST_HUMAN	xa34g05.x1 NCL_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568728 3' similar to contains L1.12 L1 repetitive element;
11121	23629	36671	1.99	9.0E-05	AI287878.1	EST_HUMAN	qv23f06.x1 NCL_CGAP_Lym8 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element
11483	18733	31486	3.89	9.0E-05	Q60716	SWISSPROT	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
11974	24939						Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G6d, G6e, G6f, G6g, G6h, G6i, G6j, G6k, G6l, G6m, G6n, G6o, G6p, G6q, G6r, G6s, G6t, G6u, G6v, G6w, G6x, G6y, G6z, G6aa, G6ab, G6ac, G6ad, G6ae, G6af, G6ag, G6ah, G6ai, G6aj, G6ak, G6al, G6am, G6an, G6ao, G6ap, G6aq, G6ar, G6as, G6at, G6au, G6av, G6aw, G6ax, G6ay, G6az, G6ba, G6bb, G6bc, G6bd, G6be, G6bf, G6bg, G6bh, G6bi, G6bj, G6bk, G6bl, G6bm, G6bn, G6bo, G6bp, G6bq, G6br, G6bs, G6bt, G6bu, G6bv, G6bw, G6bx, G6by, G6bz, G6ca, G6cb, G6cc, G6cd, G6ce, G6cf, G6cg, G6ch, G6ci, G6cj, G6ck, G6cl, G6cm, G6cn, G6co, G6cp, G6cq, G6cr, G6cs, G6ct, G6cu, G6cv, G6cw, G6cx, G6cy, G6cz, G6da, G6db, G6dc, G6dd, G6de, G6df, G6dg, G6dh, G6di, G6dj, G6dk, G6dl, G6dm, G6dn, G6do, G6dp, G6dq, G6dr, G6ds, G6dt, G6du, G6dv, G6dw, G6dx, G6dy, G6dz, G6ea, G6eb, G6ec, G6ed, G6ee, G6ef, G6eg, G6eh, G6ei, G6ej, G6ek, G6el, G6em, G6en, G6eo, G6ep, G6eq, G6er, G6es, G6et, G6eu, G6ev, G6ew, G6ex, G6ey, G6ez, G6fa, G6fb, G6fc, G6fd, G6fe, G6ff, G6fg, G6fh, G6fi, G6fj, G6fk, G6fl, G6fm, G6fn, G6fo, G6fp, G6fq, G6fr, G6fs, G6ft, G6fu, G6fv, G6fw, G6fx, G6fy, G6fz, G6ga, G6gb, G6gc, G6gd, G6ge, G6gf, G6gg, G6gh, G6gi, G6gj, G6gk, G6gl, G6gm, G6gn, G6go, G6gp, G6gq, G6gr, G6gs, G6gt, G6gu, G6gv, G6gw, G6gx, G6gy, G6gz, G6ha, G6hb, G6hc, G6hd, G6he, G6hf, G6hg, G6hi, G6hj, G6hk, G6hl, G6hm, G6hn, G6ho, G6hp, G6hq, G6hr, G6hs, G6ht, G6hu, G6hv, G6hw, G6hx, G6hy, G6hz, G6ia, G6ib, G6ic, G6id, G6ie, G6if, G6ig, G6ih, G6ii, G6ij, G6ik, G6il, G6im, G6in, G6io, G6ip, G6iq, G6ir, G6is, G6it, G6iu, G6iv, G6iw, G6ix, G6iy, G6iz, G6ja, G6jb, G6jc, G6jd, G6je, G6jf, G6jg, G6jh, G6ji, G6jj, G6jk, G6jl, G6jm, G6jn, G6jo, G6jp, G6jq, G6jr, G6js, G6jt, G6ju, G6jv, G6jw, G6jx, G6jy, G6jz, G6ka, G6kb, G6kc, G6kd, G6ke, G6kf, G6kg, G6kh, G6ki, G6kj, G6kl, G6km, G6

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2977	15593		0.71	8.0E-05	M83575.1	NT	Human platelet-derived growth factor A chain (PDGFA) gene, exons only
4579	17162	29604	1.87	8.0E-05	AW044605.1	EST_HUMAN	w778a04.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554638 3'
8683	21222	34142	0.49	8.0E-05	Y11886.1	NT	Mus musculus gene for hexokinase II, exon 1 (and joined CDS)
11030	23544	36581	2.32	8.0E-05	M69187.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
12613	24921		2.72	8.0E-05	AA276333.1	EST_HUMAN	zs88h01.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704593 3' similar to contains Alu repetitive element contains element MSR1 repetitive element ;
369	13018	25501	8.81	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA
369	13018	25502	8.81	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA
593	13223	25697	3.82	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
593	13223	25698	3.82	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
1093	13698	26208	1.41	7.0E-05	Q22649	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYL TRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2744	15299	27855	3.67	7.0E-05	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3194	15806	28278	4.69	7.0E-05	AB008080.1	NT	Dichytellum discoidium gene for TRFA, complete cds
4482	17048	29492	1.73	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4543	17127	29570	0.58	7.0E-05	U60880.1	NT	Caenorhabditis elegans Skp1p homolog mRNA, complete cds
8187	20708	33624	1.11	7.0E-05	AA505582.1	EST_HUMAN	nt93g01.s1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:966096 3'
9472	21871	34820	3.74	7.0E-05	T07095.1	EST_HUMAN	EST04984 Fetal brain, Striatum (cat#936206) Homo sapiens cDNA clone HFBED60
11040	23554		7.95	7.0E-05	10835048	NT	Homo sapiens sarcoglycan, epsilon (SGOE), mRNA
2073	14653	27225	2.03	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2073	14653	27226	2.03	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2624	15188	27753	1.34	6.0E-05	AI655241.1	EST_HUMAN	TOPOISOMERASE I (HUMAN);
2709	15268	27833	0.9	6.0E-05	Z84506.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28B10
2709	15268	27834	0.9	6.0E-05	Z84506.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28B10
2840	13329	25815	2.88	6.0E-05	AF053630.1	NT	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
5352	17912	30327	1.3	6.0E-05	AW962308.1	EST_HUMAN	EST374392 MAGG resequences, MAGG Homo sapiens cDNA
6071	18688	31432	3.12	6.0E-05	Q12660	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6071	18688	31433	3.12	6.0E-05	Q12660	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6535	19135	31928	1.45	6.0E-05	N72829.1	EST_HUMAN	y50g11.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:246212 5'
7013	19511	32332	0.79	6.0E-05	AA807680.1	EST_HUMAN	q80a03.s1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:1504588 3'
8026	20571	33475	0.97	6.0E-05	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h08 BT0311 Homo sapiens cDNA
8026	20571	33476	0.97	6.0E-05	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-h08 BT0311 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8381	20921	33841	0.65	6.0E-05	AA150482.1	EST_HUMAN	208c08.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:491726 3' similar to contains element MER28 repetitive element ;
8385	20925	33845	2.3	6.0E-05	AW686629.1	EST_HUMAN	PM4-NN0050-310300-001-110 NN0050 Homo sapiens cDNA
8516	21055	33978	0.62	6.0E-05	Q60401	SWISSPROT	COMPLEMENT DECA-ACCELERATING FACTOR PRECURSOR
9176	21753	34698	1.09	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9176	21753	34700	1.09	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9440	21966	34915	1.13	6.0E-05	T94149.1	EST_HUMAN	ye28c12.r1 Stralagene lung (#637210) Homo sapiens cDNA clone IMAGE:119062 5'
9637	22137	35103	0.57	6.0E-05	AW627985.1	EST_HUMAN	h137a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2874444 3'
10627	23159	36172	3.96	6.0E-05	R75639.1	EST_HUMAN	y69408.s1 Soares_pleocenta_NbZHP Homo sapiens cDNA clone IMAGE:143535 3' similar to contains Alu repetitive element; contains LTR repetitive element ;
11394	23846	36811	4.18	6.0E-05	AA044015.1	EST_HUMAN	zk68f02.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487035 5'
12193	24919	30716	10.26	6.0E-05	AW690110.1	EST_HUMAN	MRC-NT0038-250400-001-409 NT0038 Homo sapiens cDNA
1449	14041	26569	18.37	5.0E-05	AW392086.1	EST_HUMAN	QV4-ST0234-241189-040-111 ST0234 Homo sapiens cDNA
1903	14488		1.75	5.0E-05	8923891	NT	Homo sapiens 22kDa peroxidomal membrane protein-like (LOC55895), mRNA
4051	16648	29116	3.86	5.0E-05	AJ251894.1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
5716	18342	30848	11.26	5.0E-05	X68855.1	NT	Human ML C1emb gene for embryonic myosin alkaline light chain, 3'UTR
6144	18758	31516	2.97	5.0E-05	AW653544.1	EST_HUMAN	AV653544 GLC Homo sapiens cDNA clone GLCMA06 3'
6316	18823	31700	0.97	5.0E-05	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
7370	19896		1.22	5.0E-05	AB037864.1	NT	Mus musculus gene for calretinin, exon 1
11971	24460		5.73	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
12249	24460		9.18	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2833	12806		3.49	4.0E-05	U12821.1	NT	Human renin (REN) gene, 5' flanking region
4580	17163	28605	1.37	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4580	17163	28606	1.37	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
5166	17735	30162	0.58	4.0E-05	AF212313.1	NT	Drosophila melanogaster senseless protein (sens) gene, complete cds
7020	19518	32340	0.75	4.0E-05	U01947.1	NT	Macaca mulatta haptoglobin (HP) gene, 5' region
9442	21968		7.26	4.0E-05	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
9812	22408	35364	0.55	4.0E-05	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
10305	22799	35790	0.73	4.0E-05	P23760	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE) (ACID BETA-GALACTOSIDASE)
10648	23180	36163	5.05	4.0E-05	AW627946.1	EST_HUMAN	h196c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2874380 3' similar to contains element MIR repetitive element ;
11850	24210	31041	3.27	4.0E-05	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
11929	24264		1.38	4.0E-05	AW117580.1	EST_HUMAN	xd83e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2805192 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
709	13330	25817	0.64	3.0E-05	A1248061.1	EST_HUMAN	qh84c10.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element.
1097	13702	26212	1.49	3.0E-05	AW273851.1	EST_HUMAN	xv24g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1170	13772	26280	1.51	3.0E-05	BF037898.1	EST_HUMAN	601461463F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3885142 5'
1170	13772	26281	1.51	3.0E-05	BF037898.1	EST_HUMAN	601461463F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3885142 5'
2748	15301	27867	1.17	3.0E-05	Q62234	SWISSPROT	SKELEMIN
3331	15941		0.89	3.0E-05	A1288919.1	EST_HUMAN	q191g11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1879748 3' similar to TR:O08632
4471	17057	29503	7.22	3.0E-05	BE169211.1	EST_HUMAN	O08632 GLYCINE TYROSINE-RICH HAIR PROTEIN.
4471	17057	29504	7.22	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4565	17148	29594	1.08	3.0E-05	AA388679.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4565	17148	29595	1.08	3.0E-05	AA388679.1	EST_HUMAN	EST79986 Placenta 1 Homo sapiens cDNA similar to similar to p53-associated protein
4692	17274		0.71	3.0E-05	AL163302.2	NT	EST79986 Placenta 1 Homo sapiens cDNA similar to similar to p53-associated protein
4728	17307	29751	0.75	3.0E-05	AF149773.1	NT	Homo sapiens chromosome 21 segment HS21C102
4963	13330	25817	0.65	3.0E-05	A1248061.1	EST_HUMAN	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
5746	18372	31080	1.73	3.0E-05		NT	qh84c10.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element.
6854	19442	32257	1.28	3.0E-05	AJ225782.1	NT	Mus musculus myosin light chain 2, precursor lymphocyte-specific (Myo2pl), mRNA
6854	19442	32258	1.28	3.0E-05	AJ225782.1	NT	Homo sapiens SYBL1 gene, exons 6-8
7839	20381	33286	1.9	3.0E-05	BE733157.1	EST_HUMAN	Homo sapiens SYBL1 gene, exons 6-8
8293	20834	33756	1.29	3.0E-05	AA284049.1	EST_HUMAN	601587451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842282 5'
8824	21363	34288	1.76	3.0E-05	AW770982.1	EST_HUMAN	zs60b05.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:701841 3'
8828	21387	34291	1.22	3.0E-05		NT	h194d08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009638 3'
8832	21371	34298	0.47	3.0E-05	P43361	SWISSPROT	Homo sapiens interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA
9058	21595		0.88	3.0E-05	X03273.1	NT	MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN)
9244	21770	34718	1.3	3.0E-05	AA372562.1	EST_HUMAN	Human Alu-family cluster 5' of alpha(1)-acid glycoprotein gene
9581	22081		2.97	3.0E-05	A1769331.1	EST_HUMAN	EST84475 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
10428	22922	35925	0.85	3.0E-05	Q62918	SWISSPROT	wg36f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2387208 3'
10428	22922	35926	0.85	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
12055	24338		1.48	3.0E-05	AJ271735.1	NT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
12387	25101		1.52	3.0E-05	AW518689.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region, segment 1/2
2362	14933	27506	1.55	2.0E-05	A1286021.1	EST_HUMAN	xs89d06.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:2776811 3'
2819	15181	27747	10.26	2.0E-05	M13792.1	NT	qh98e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element.
							Human adenosine deaminase (ADA) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2738	15293		6.76	2.0E-05	AA160562.1	EST_HUMAN	zq46a12.r1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains Alu repetitive element; contains element L1 repetitive element ;
3171	15785	28257	1.59	2.0E-05	BE066036.1	EST_HUMAN	RC3-BT0319-120200-014-H08 BT0319 Homo sapiens cDNA
3391	15989	28477	0.83	2.0E-05	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3416	16024	28506	1.04	2.0E-05	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
3541	16146		0.72	2.0E-05	X85465.1	NT	S. cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
3880	16478		0.67	2.0E-05	AL039107.1	EST_HUMAN	DKFZp5681064_r1 568 (synonym: hifad2) Homo sapiens cDNA clone DKFZp5681064 5'
5010	17583	30026	0.63	2.0E-05	AJ131016.1	NT	Homo sapiens SCL gene locus
5176	17743		2.42	2.0E-05	L77689.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
5933	18555	31282	1.64	2.0E-05	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
6125	18740	31492	1.4	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6125	18740	31493	1.4	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6305	18912	31686	0.73	2.0E-05	AH49272.1	EST_HUMAN	qc72a02.x1 Soares_placenta_8to9weeks_2NbHP8tc9W Homo sapiens cDNA clone IMAGE:1715114 3'
6736	19330	32136	2.12	2.0E-05	AA714330.1	EST_HUMAN	similar to contains L1.13 L1 repetitive element ;
6982	19480	32301	2.2	2.0E-05	Y08926.1	NT	nm06d12.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238519 3'
6994	19492	32313	1.34	2.0E-05	A1492960.1	EST_HUMAN	P.falcipterum mRNA for AARP1 protein, partial
7002	19500		8.08	2.0E-05	A1891025.1	EST_HUMAN	qz47b06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2030003 3' similar to TR:O02711
							O02711 PRO-POLYDUTPASE POLYPROTEIN ;
							wu35h07.x1 Soares_Dieckgraebe_color_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
7207	19738	32591	2.2	2.0E-05	AF224262.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7207	19738	32592	2.2	2.0E-05	AF224262.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7403	19928		0.91	2.0E-05	AF128847.1	NT	Homo sapiens indolethylamine N-methyltransferase (INMT) mRNA, INMT-2 allele, complete cds
7826	20368	33276	1.41	2.0E-05	A1381040.1	EST_HUMAN	ig20h05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109369 3'
9191	21708	34651	0.49	2.0E-05	P49457	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
9191	21708	34652	0.49	2.0E-05	P49457	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
9837	22335	35317	0.48	2.0E-05	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
10041	22536	35532	0.74	2.0E-05	BF056939.1	EST_HUMAN	7175g09.y1 NCI_CGAP_Bm20 Homo sapiens cDNA clone IMAGE:3340576 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10482	22976	35984	2.62	2.0E-05	N41751.1	EST_HUMAN	yw91a06.r1 Soares_placenta_8to9weeks_2NHP8b9W Homo sapiens cDNA clone IMAGE:259570 5'
10482	22976	35985	2.62	2.0E-05	N41751.1	EST_HUMAN	yw91a06.r1 Soares_placenta_8to9weeks_2NHP8b9W Homo sapiens cDNA clone IMAGE:259570 5'
10524	19500		2.44	2.0E-05	A1981025.1	EST_HUMAN	wu35h07.x1 Soares_Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
11327	23025	36034	2.74	2.0E-05	BE175801.1	EST_HUMAN	RC5-HT0582-280300-012-E12 HT0582 Homo sapiens cDNA
11883	24844		4.91	2.0E-05	BE348228.1	EST_HUMAN	hw21a03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3183532 3' similar to TR:Q12832 Q12832 GLYCOPHORIN HEP2
12090	25018		13.02	2.0E-05	AW074604.1	EST_HUMAN	xa69a03.x1 NCI_CGAP_Co17 Homo sapiens cDNA clone IMAGE:2573932 3' similar to contains L1.b3 L1 repetitive element
12144	24831		2.54	2.0E-05	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
12655	24727		2.35	2.0E-05	A1200970.1	EST_HUMAN	qf68g11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1756236 3'
2719	15475	27841	1.45	1.0E-05	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
3711	16312	28780	1.91	1.0E-05	AF088273.1	NT	Drosophila melanogaster strain Lantio 120 Suppressor of Hairless (Su(H)) gene, partial cds
4039	16637	29105	11.9	1.0E-05	P61274	SWISSPROT	MOSAIC PROTEIN LGN
4252	16840	29289	0.98	1.0E-05	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4364	16951	29391	1.89	1.0E-05	AA431119.1	EST_HUMAN	zw69g04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781494 5'
4976	17550	29692	2.24	1.0E-05	AW419134.1	EST_HUMAN	xy49g11.x1 NCI_CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
5395	17953		0.94	1.0E-05	A173556.1	EST_HUMAN	os64d07.x5 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1610125 3' similar to contains Alu repetitive element
5426	17983	30388	0.91	1.0E-05	L27595.1	NT	Mus muscaris bradykinin B2 receptor (B2R) gene, complete cds
6848	19438	32252	1.32	1.0E-05	A1246003.1	NT	Homo sapiens Spast gene for spastin protein
7140	19520	32342	3.98	1.0E-05	AA641846.1	EST_HUMAN	ns18g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.t1 L1 L1 repetitive element
7142	19675	32515	14.32	1.0E-05	4505844	NT	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
7655	20167	33054	0.76	1.0E-05	BF222646.1	EST_HUMAN	7p57d01.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3849945 3' similar to contains MER10.b3 MER10 repetitive element
7754	20282		2.22	1.0E-05	P19474	SWISSPROT	S2 KD RO PROTEIN (SJOJGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
8846	21385		2.56	1.0E-05	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8990	21528	34457	2.18	1.0E-05	AA452578.1	EST_HUMAN	zc35h12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788519 3' similar to gb:U02902 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
9211	21728	34671	13.74	1.0E-05	AA236110.1	EST_HUMAN	zs05a11.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684332 5' similar to contains Alu repetitive element; contains element TAR1 repetitive element
9288	21888	34634	0.6	1.0E-05	AV732190.1	EST_HUMAN	AV732190 HTF Homo sapiens cDNA clone HTFBIH01 5'

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9752	22250	35232	0.76	1.0E-05	AW510902.1	EST_HUMAN	hd41b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains OFR.I1 OFR repetitive element;
9752	22250	35233	0.76	1.0E-05	AW510902.1	EST_HUMAN	hd41b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912043 3' similar to contains OFR.I1 OFR repetitive element;
9830	22328	35309	1.58	1.0E-05	AW291521.1	EST_HUMAN	UI-H-B12-agg-k-08-0-J1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
9830	22328	35310	1.58	1.0E-05	AW291521.1	EST_HUMAN	UI-H-B12-agg-k-08-0-J1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
10087	22582		1.73	1.0E-05	AW469895.1	EST_HUMAN	ha07c10.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1.12 L1 repetitive element;
10799	23322	36332	2.32	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
10799	23322	36333	2.32	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12493	25011	30616	1.67	1.0E-05	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2696	15253	27824	4.74	9.0E-06	AI583811.1	EST_HUMAN	h73a06.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246386 3'
3130	15744	28213	5.23	9.0E-06	AI218983.1	EST_HUMAN	gg11b08.x1 Soares_placenta_8to9weeks_2NHP8606SW Homo sapiens cDNA clone IMAGE:1759191 3'
3670	16271		3.37	9.0E-06	M81755.1	NT	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
6084	18681	31423	2.25	9.0E-06	L23416.1	NT	Homo sapiens differentiation antigen CD20 gene, exons 5, 6
6947	19524	32346	0.84	9.0E-06	BE065042.1	EST_HUMAN	RC1-BT0313-110500-017-a07 BT0313 Homo sapiens cDNA
7466	19988	32853	0.85	9.0E-06	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7751	20259	33156	12.47	9.0E-06	AI034370.1	EST_HUMAN	ox20g01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1658912 3' similar to contains Alu repetitive element;
8400	20840	33883	1.18	9.0E-06	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
8913	21451	34372	2.48	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
8913	21451	34373	2.48	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9149	21694	34628	4.6	9.0E-06	U35114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
10818	23339	35353	3.78	9.0E-06	Q10364	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
2589	15469	27701	1.48	8.0E-06	AW362539.1	EST_HUMAN	RC3-CT0283-201199-011-rt11 CT0283 Homo sapiens cDNA
10424	22918	35919	0.64	8.0E-06	P34083	SWISSPROT	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
10424	22918	35920	0.64	8.0E-06	P34083	SWISSPROT	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)

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1015	13625		1.71	7.0E-06	AA669728.1	EST_HUMAN	ab90f10.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains
1487	14080	26619	3.36	7.0E-06	7682177	NT	MER20.11 MER20 repetitive element ; Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2177	14754	27324	1.55	7.0E-06	AW593215.1	EST_HUMAN	hg11b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945279 3' similar to gb:X62048_cds1 WEE1-LIKE PROTEIN KINASE (HUMAN);
2897	15514		7.94	7.0E-06	A1368252.1	EST_HUMAN	qw16g09.x1 NCL_CGAP_U13 Homo sapiens cDNA clone IMAGE:1991286 3' similar to contains Alu repetitive element;
3620	16223		1	7.0E-06	AA3385542.1	EST_HUMAN	EST99205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat
5874	18486		5.81	7.0E-06	AW883141.1	EST_HUMAN	QV2-O.T0062-250400-173-h01 OT0082 Homo sapiens cDNA
5972	18593	31327	0.94	7.0E-06	NB8645.1	EST_HUMAN	y65cd7.r1 Soares_multiple_sclerosis_2NbHMSHP Homo sapiens cDNA clone IMAGE:278412 5'
8724	21263	34183	0.72	7.0E-06	11420709	NT	Homo sapiens DNA segment, numerous copies, expressed probes (GS1 gene) (DXF68S1E), mRNA
9814	22312		2.32	7.0E-06	Q61147	SWISSPROT	CERULOPLASMIN PRECURSOR (FERROXIDASE)
11710	25043	30506	1.62	7.0E-06	BF215972.1	EST_HUMAN	601881522F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4063972 5'
2842	15558	28032	1.29	6.0E-06	BE069189.1	EST_HUMAN	QV3-B.T0379-010300-105-d11 BT0379 Homo sapiens cDNA
4865	15584	28065	2.03	6.0E-06	Q01456	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
4875	17450	28901	1.47	6.0E-06	A1040099.1	EST_HUMAN	ox08602.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to contains MER6.t2 MER8 repetitive element ;
5582	18184	30589	1.3	6.0E-06	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
5605	18234	30685	1.15	6.0E-06	Q02040	SWISSPROT	PROTEIN XE7
9770	22288		1.67	6.0E-06	AW801912.1	EST_HUMAN	IL5-UM0070-110400-063-g02 UM0070 Homo sapiens cDNA
12602	24688	30881	1.47	6.0E-06	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
5361	17921	30335	1.02	5.0E-06	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C088
6211	18821	31582	3.73	5.0E-06	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6479	19080	31863	2.04	5.0E-06	U07561.1	NT	Human ABL gene, exon 1b and Intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
7284	19812	32688	1.11	5.0E-06	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds
10013	22508	35489	6.57	5.0E-06	AA313620.1	EST_HUMAN	EST185496 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
10406	22900	35895	0.54	5.0E-06	P06881	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
12482	24615	30890	13.8	5.0E-06	A1065045.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA
675	13289	25780	6.05	4.0E-06	R16267.1	EST_HUMAN	ye48c03.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element; contains L1 repetitive element ;
879	13483	26011	6.94	4.0E-06	AW103354.1	EST_HUMAN	xc69g12.x1 NCL_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu repetitive element; contains element MER21 repetitive element ;